

CREATION RESEARCH SOCIETY



QUARTERLY

Volume 53 Summer 2016 Number 1

- **NEUTRON STARS IN GLOBULAR CLUSTERS:
EVIDENCE OF YOUNG AGE?**
- **COMETS, THE KUIPER BELT, AND THE OORT CLOUD**
- **APPARENT AGE OF THE TIME-DILATED UNIVERSE—PART II**
- **CELLS AS INFORMATION PROCESSORS—PART II"**

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Haec Credimus

For in six days the Lord made heaven and earth, the sea, and all that in them is, and rested on the seventh. —Exodus 20:11

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Editorial

The Previous Issue and an Overview of this Issue

I am sure many of you have had the chance to read the previous issue of the *Creation Research Society Quarterly*, an issue dedicated to genetics. We have had many positive comments about it, as we did with the preceding special issue a year earlier on the iDINO project. We hope that dedicating the spring issue to a theme becomes an annual event. The spring 2017 issue will explore astronomy.

Speaking of special issues and astronomy, we have related articles in this issue. First, Part I of Royal Truman's article, "Cells as Information Processors," appeared in the genetics issue. I am pleased that the second part of his work is featured in this issue. Perhaps as a sort of unintended lead-up to our next special spring issue, we have three astronomy articles in this issue. One article is by the well-known creation scientist, John Hartnett, who wrote "Comets, the Kuiper Belt, and the Oort Cloud." This one is close to my interests, because I have written on these subjects in the past. An-

other article, "The Apparent Age of the Time-Dilated Universe," is by Creation Research Society board member and my research partner, Ron Samec. The third article, "Neutron Stars in Globular Clusters: Evidence of Young Age?" is by first-time *Creation Research Society Quarterly* author, Paul Nethercott.

This issue also features the abstracts of presentations given at the Sixth Meeting of the Creation Research Society held on the campus of Concordia University in Ann Arbor, Michigan, July 28–30. This meeting had the greatest attendance yet (130 participants), and I personally think the presentations were the best ever. We continue to strive to improve our meetings, and so I am sure the next meeting scheduled on the campus of Bob Jones University in Greenville, South Carolina, July 27–29, 2017, will be even better. These are *the* meetings of the Creation Research Society, so every member ought to make attendance a priority. By attending meetings, we can catch up on the work other Society

members are doing. But in addition, the fellowship and networking opportunities are tremendous as well. I hope to see many of you at the Seventh Meeting.

We also have some interesting letters to the editor in this issue. Letters to the editor in the *Creation Research Society Quarterly* typically have been in response to articles published in previous issues, but there is no reason why they ought to be restricted to that. For instance, in this issue, B. T. Mann brings up some interesting points for discussion dealing with the effects of Adam's sin upon the creation. What he has to say, while probably too short for an article, certainly is worth bringing to others' attention, so it seems ideal for the subject of a letter. I would like to see future letters of this sort.

Danny R. Faulkner
Editor
*Creation Research
Society Quarterly*

Comets, the Kuiper Belt and the Oort Cloud

John G. Hartnett*

Abstract

With the development of modern space-based telescopes and the past decade or more of collection of data on both comets and celestial bodies found to orbit the sun at distance greater than that of the planet Neptune, a review of the current data suggests that there can be no longer any doubt that the Kuiper belt does exist. However, the objects contained therein probably more properly should be called trans-Neptunian objects because there is no reason that the solar system ends at Neptune and a new region of space begins. On the other hand, there is no evidence that the putative Oort cloud exists. The Kuiper belt was originally believed to be the primary source from which the Oort cloud was populated over the alleged 4.6-billion-year history since our solar system formed. The latter still has not been found, yet it is critically needed as the only source of long-period comets for the uniformitarian theory. However, I suggest that the existence of short-period comets as a young solar system argument may no longer be tenable.



Figure 1. Comet C/2012 S1 (ISON) April 30, 2013. The comet was 3.9 AU (580 million km) from the sun and 4.3 AU (640 million km) from Earth. Photo from NASA/Hubblesite.org

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Introduction

Comets were once thought to be atmospheric phenomena, and there was a time when they were believed to be harbingers of doom (Sarfati, 2003). Comets are now known to be dirty balls of ice and dust and some even icy dirt balls (Hartnett, 2006). They travel into the inner solar system displaying, in some cases spectacularly, their long tails, which comprise escaping gas and dust, the result of ices sublimating¹ from their icy surface. This display gets stronger as they approach the sun, where the sun's radiation has a very strong effect on the volatile chemicals in the ball of ice. Driven away from the sun by radiation pressure and the solar wind, this loss of material depletes the mass of the comet. Some comets have relatively short orbital periods of less than 200 years, whereas others have periods much longer than 200 years. This has become a convenient basis for classifying a comet short-period or long-period. However, the more significant criteria of classification are their orbital characteristics: inclination and whether prograde or retrograde in their orbital trajectories.

The Bible gives an age of the solar system and the universe of around 6000 years, but the nebular hypothesis proposes that the solar system began condensing from a giant collapsing cloud of molecular hydrogen (Hartnett, 2016a) and dust about 5 billion years ago and that the material of comets formed about 4.6 billion years ago. Based on the known loss rate of the material from observed comets, however, there should be no short-period comets left (Faulkner, 1997, 2001).

A typical comet nucleus (5–10 km in diameter) has a mass of $5\text{--}10 \times 10^{14}$ kg. That may seem like a lot, but comets

lose tens of tons of material per second on approach to the sun. Comet Halley at its peak loss rate loses about 54 tons/second of gas, including gas from volatile ices, at a distance of about 1 AU² from the sun. Assuming the process occurs only during one third of its orbit—the portion when it is closest to the sun—a comet loses about 5.7×10^{11} kg/passage, which means it could survive only 95 passages around the sun before there is no matter left (Vanderbilt University, 2016).

Assuming that a comet is sourced from the original material from the creation of the solar system, if it passes the sun once in 200 years, it could pass only 30 times in the biblical lifetime of the solar system, which is completely within expectation. In fact, it would only be 30% depleted of its initial mass. That means it still would have 65 more passages left before all the material from its nucleus would be lost. But how could it pass 25 million times as required in the uniformitarian lifetime of the solar system? There is the problem. Why do short-period comets still exist if the nebular hypothesis is the true description of the formation of the solar system? Quite obviously this problem does not exist for the biblical creationist.

Long-period comets might have a period from a hundred thousand years up to a million years, it is alleged. But if they too can survive only 95 passages around the sun, they have at most only 95 million years of total life.³ So, why are there still any long-period comets? From the perspective of the uniformitarian nebular hypothesis, where do they come from?

The Kuiper Belt

One commonly used university astrophysics text (Carrol and Ostlie, 2007, p. 717) reports:

From their orbital characteristics, it seems very likely that the present-day source of the short-period comets is the **Kuiper belt**, a collection of icy objects located predominantly near the plane of the ecliptic and beyond the orbit of Neptune, typically ranging from 30 AU to perhaps 1000 AU or more from the Sun. It is now realized that Pluto and its moon Charon, 2003 UB313, Sedna, and Quaoar are among the largest known members of the family of **Kuiper belt objects** (KBOs), also referred to as **Trans-Neptunian Objects** (TNOs).

The Kuiper belt (KB) is a doughnut-shaped region of space beyond the orbit of the planet Neptune wherein there have now been observed on the order of 2000 bodies orbiting the sun. In reality these should be simply referred to as trans-Neptunian objects (TNOs) because there is no good reason to suppose that our solar system abruptly stops at the orbit of Pluto. The first KBO, 1992 QB1, was detected in 1992. Other large bodies comparable in size to Pluto have been found since—for example, Charon, Eris (Jet Propulsion Laboratory, 2016), Sedna, and Quaoar (See Table I). One of these, Eris, discovered in 2003, is slightly smaller in size than Pluto but more massive, yet Pluto was counted as one of the planets at that time. This was one of the reasons in 2006 Pluto was reclassified to being one of the minor planets.

I think we can definitely say that the Kuiper belt of bodies with masses comparable to Pluto's and smaller does exist beyond the orbit of Neptune. The question then remains: Is the Kuiper belt a solution to the problem of short-period comets (Newton, 2002, pp. 15–17)?

¹ Sublimation is the transition a substance undergoes when directly changing from the solid phase to the gas phase without passing through the intermediate liquid phase.

² 1 AU = 1 astronomical unit = the distance from the earth to the sun, about 150 million km.

³ This is only 2% of the alleged age of the solar system of 5 billion years. It represents an upper limit only, which is much less than the alleged 5-billion-year age.

Name	Diameter (km)	Period (yr)	a (AU)	e	s (deg) [†]
Eris	2400	559	67.89	0.4378	43.99
Pluto	2274	248	39.48	0.2488	17.16
Sedna*	1600	12,300	531.7	0.857	11.93
Orcus	1500	247	39.39	0.220	20.6
Charon	1270	248	39.48	0.2488	17.16
2005 FY9	1250	309	45.71	0.155	29.0
2003 EL61	1200	285	43.34	0.189	28.2
Quaoar	1200	287	43.55	0.035	8.0
Ixion	1070	249	39.62	0.241	19.6
Varuna	900	282	42.95	0.052	17.2
2002 AW197	890	326	47.37	0.131	24.4

* Sedna has a highly eccentric orbit which is much larger than the classical Kuiper belt.

[†] The parameters a , e , and i represent, respectively, the semi-major axis, eccentricity and inclination of their orbits. Table I is reproduced from (Carrol and Ostlie, 2007).

Table I. A list of the largest known Kuiper Belt objects as of May 2006. Many of the listed diameters are quite uncertain.

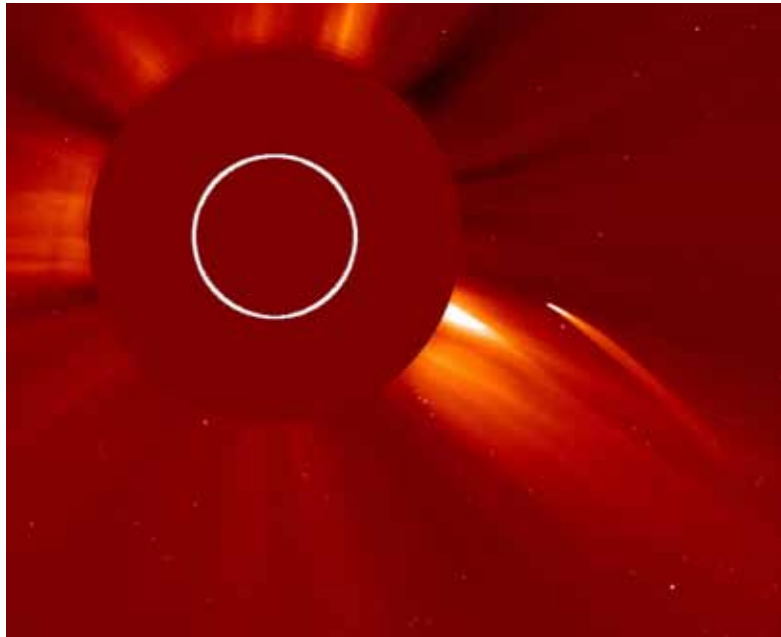


Figure 2. An image of a comet plunging into the sun (right-hand side). The disk of the sun is covered so that the sun's corona and coronal mass ejections can be studied. The image was obtained by the LASCO instrument onboard SOHO on July 5 and July 6, 2011. As of 2015 SOHO has discovered 3000 comets this way. Image from ESA/NASA/SOHO.

Observed Comets in the Solar System

To add to the loss-of-mass problem for comets, making it even worse than stated above, while some comets approaching the sun

suffer relatively small amounts of sublimation near perihelion compared with their masses, other comets may experience more severe consequences. For instance, when Comet West moved through the inner Solar System in 1976, its nucleus broke into four separate pieces. Comet Kohoutek also split apart in 1974. Perhaps more impressive are the **Sun-grazing comets**. While it has been intensely studying the Sun, the LASCO instrument onboard the SOHO spacecraft has discovered more than 1000 comets that make close approaches to the Sun. In some instances, the comets' orbits cause them to plunge into the Sun, as occurred with Comet SOHO-6. (Carrol & Ostlie, 2007, p. 825)

As of the time of writing this article, the ESA/NASA Solar Heliospheric Observatory (SOHO) spacecraft has catalogued 3,000 comets (Wall, 2015). Some of them were observed plunging into the sun, as shown in Figure 2. The SOHO satellite has permitted an enormous number of sun-grazing (including sun-diving) comets to be detected. One class of those comets are Kreutz comets, which all seem to have approximately the same orbit and appear to be from the past breakup of a larger comet.

Why Are We Seeing So Many Sun-grazing Comets?

A NASA video available on YouTube (<https://youtu.be/2u73bIzg5CU>) offers an answer to this question.

Before 1979, there were less than a dozen known sun-grazing comets—comets that swing by incredibly close to the sun. But that was before the ESA/

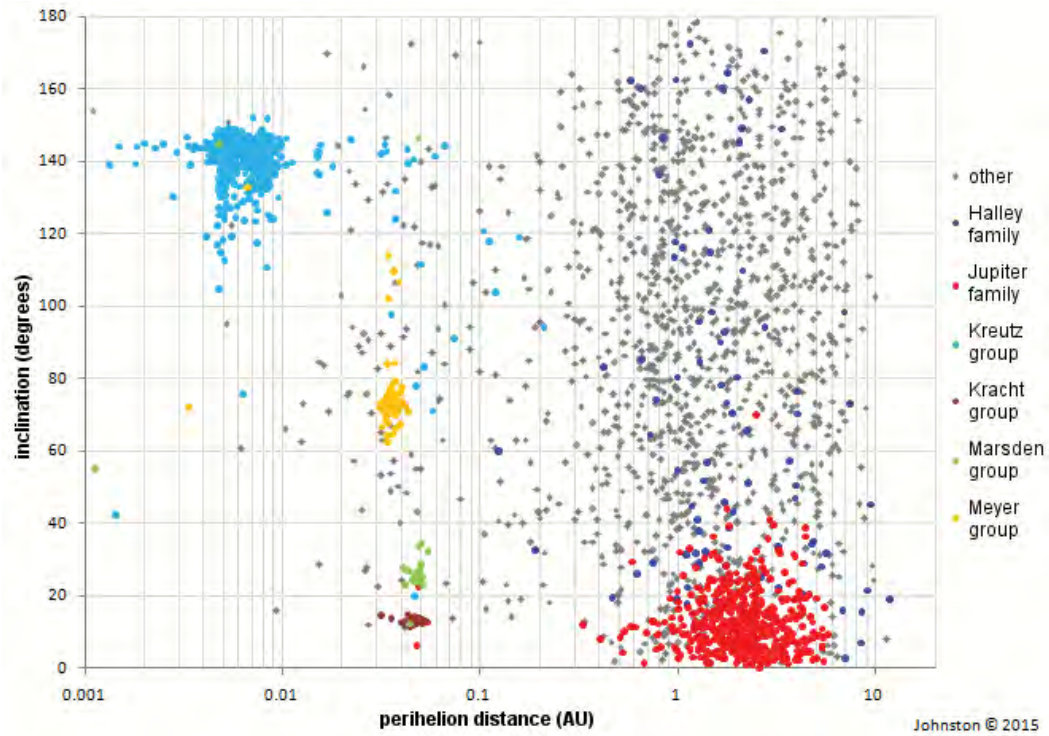


Figure 3. Inclination versus perihelion distance for 3,821 comets. Reproduced from Johnston (2015a).

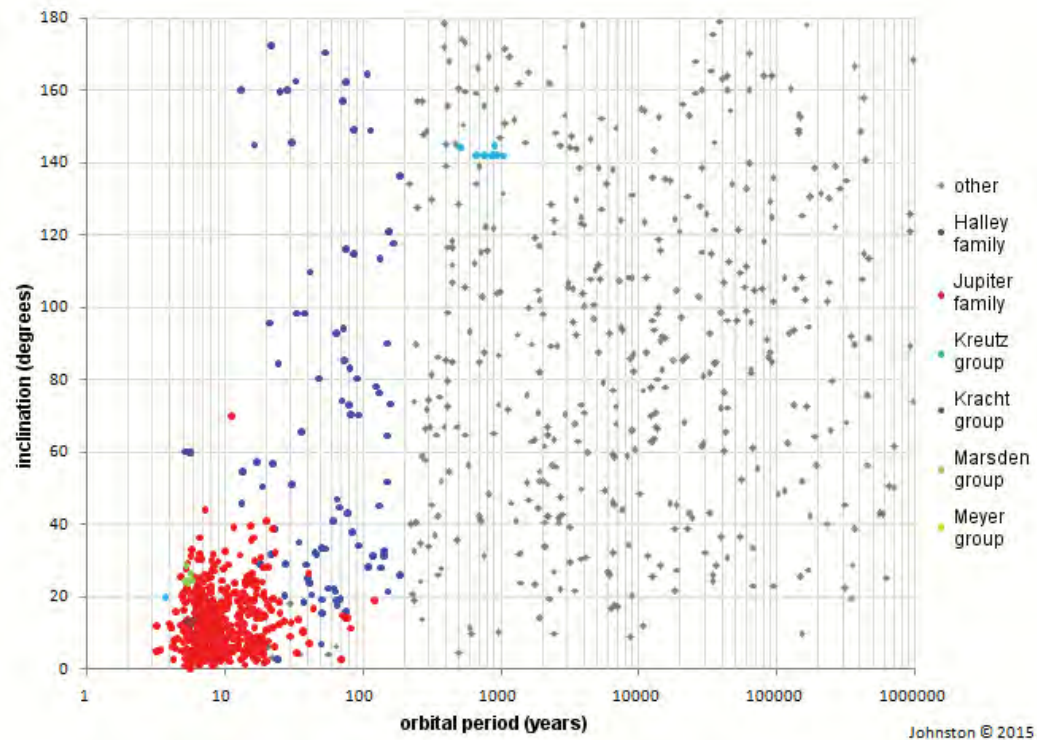


Figure 4. Inclination versus orbital period for 1,152 comets. Reproduced from Johnston (2015a).

NASA SOHO spacecraft was launched in 2000. Since then, SOHO has become the greatest sun-grazing comet hunter of all time, with a current comet find of 3000.

The existence of so many sun-grazing comets again shows the fragility of comets, which means the supply of comets will be depleted even faster than any uniformitarian calculation would indicate. Consider the following quote:

The overwhelming bulk—some 85 percent—of SOHO’s comet discoveries are what’s [sic] called Kreutz comets. Scientists think a single extremely large sun-grazing comet broke up thousands of years ago, leading to thousands of leftover fragments, which continue to follow the same Kreutz path. On average, a new member of the Kreutz family is discovered every three days. Unfortunately, the long journey for these fragments invariably ends as they pass the sun. If they’re close enough to the sun to be seen by SOHO, they’re too close to survive.

“They just disintegrate every time we observe one,” said Karl Battams, a solar scientist at the Naval Research Labs in Washington, D.C., who has been in charge of running the SOHO comet-sighting website since 2003. “There’s only one Kreutz comet that made it around the sun—Comet Lovejoy. And we are pretty confident it fell apart a couple of weeks afterwards.” (Fox, 2015)

Some sun-grazing comets have been discovered after getting around the sun, but most sun-grazers do not make it past. Figure 3 shows the inclination (i) versus the perihelion distance⁴ for 3821 comets (Johnston, 2015a). The Kreutz family

are closely grouped (light blue dots in Figure 3) at very similar inclinations to the plane in which the planets orbit (the ecliptic), and they have similar perihelion distances, very close to the sun.

Figure 4 illustrates, using different colors, the different families of comets, most of which have been discovered since 1990. The Jupiter family (red dots in Figure 4) are a class of comets that have orbits where they pass within 1 AU and 5 AU at perihelion and have aphelion between the orbits of Jupiter (5 AU) and Saturn (10 AU), and orbital periods less than 200 years. They all have very low inclinations, which means they essentially orbit in the plane of the planets. The well-known Halley family (dark blue dots in Figure 4) have orbital periods mostly from 10 to 200 years. Above 200 years, we clearly see the long-period comets, which are plotted in Figure 4 as grey diamonds and a few light-blue dots. The Kreutz group that there is data for (light-blue dots) have orbital periods between 500 and 800 years, which also makes them long-period comets. The Halley family and the Kreutz family and the other long-period comets have a whole range of orbital inclinations, which means they form a spherical cloud around the sun.

The Oort Cloud

And what about the long-period comets? They

apparently originate in the **Oort cloud**, an approximately *spherically symmetric cloud of cometary nuclei* with orbital radii of between 3000 and 100,000 AU. Having spent most of their existence in “deep freeze” at the outer reaches of the Solar System, comets and Kuiper belt objects appear to be ancient remnants of its formation, although perhaps not entirely unaffected by nearly 4.6 billion years of exposure to the environment of space. (Carroll and Ostlie, 2007, p. 717, emphasis added)

The textbook argument is now being made that long-period comets and Kuiper belt objects originate from the Oort cloud. See Figure 5. This includes Kuiper belt objects. Hence the KB’s existence is now being linked to an unobserved spherical halo of trillions of icy cometary nuclei, which was proposed only because of the observed existence of comets, both short and long period, in an alleged 4.6-billion-year-old solar system.

In 1950, based on a very careful statistical study of their apparently random orbits, Jan Oort (1900–1992) concluded that long-period comets originate in a distant distribution of cometary nuclei now known as the **Oort cloud**. *Although the Oort cloud has never been observed*, its existence seems certain. As we noted [above], the reservoir of nuclei appears to be located between 3000 AU and 100,000 AU from the Sun and probably contains 10^{12} – 10^{13} members with a total mass on the order of 100 $M_{\oplus}$. For comparison, the nearest stars are approximately 275,000 AU away. The inner Oort cloud (3000 AU to 20,000 AU) may be slightly concentrated along the ecliptic, while the outer Oort cloud (20,000 AU to 100,000 AU) has a *nearly spherical distribution of cometary nuclei*. (Carroll and Ostlie, 2007, p. 825–826, emphasis added)

The alleged structure of the unseen Oort cloud is described, but that has been based on the believed evolutionary theory of the formation of the solar system (Hartnett, 2016a, 2016b). Since there still does not exist any observational evidence for the Oort cloud, it remains as evolutionary storytelling.

As of 2016, no Oort cloud has been detected, yet 1,947 TNOs, centaurs, and scattered disk objects (SDOs) are now identified (Johnston, 2015b). Centaurs are fairly large icy bodies that orbit the sun but are not classed as comets, though some say they may become

⁴ Perihelion distance is the comet’s closest approach to the sun while the aphelion distance is its greatest distance on its path in an elliptical orbit.

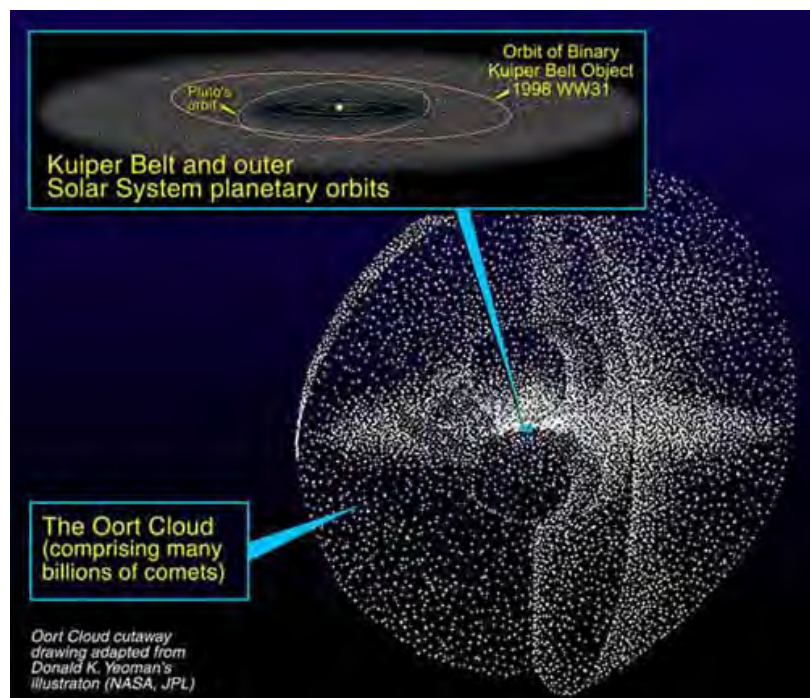


Figure 5. The alleged Oort cloud with the Kuiper belt inset. Image from NASA via Wikipedia.

short-period comets if they are knocked out of their current orbits.

As detections have increased, KBOs have been classed into three different groups based on their orbital characteristics. **Classical KBOs** are those that orbit between 30 AU (Neptune's distance) and 50 AU from the sun, with orbital inclinations less than about 30°. Then there are **Scattered KBOs** with much higher orbital eccentricities. Eris (2003 UB313) is one example of a scattered KBO. The perihelion distances of scattered KBOs are around 35 AU, and they have greater orbital inclinations than classical KBOs. Scattered KBOs are suggested as another source of the short-period comets. Lastly, a class of **resonant KBOs** exists that has orbital resonances with Neptune. Pluto is locked in a 3:2

orbital resonance⁵ with Neptune that protects it from ever colliding with the ice giant. As a result, Pluto (and its binary partner Charon) are resonant KBOs. Any KBOs that have 3:2 orbital resonances with Neptune are referred to as Plutinos (see Figure 6). Many other different orbital resonances have been observed for KBOs as well (Carroll and Ostlie, 2007; Johnston, 2015c). Figure 6 shows many classical, scattered, and resonant KBOs.

Figure 7 plots known KBOs and inner solar system bodies (inside the orbit of Uranus at semimajor axis of 19 AU). This is data from September 8, 2005, but it clearly shows many

⁵ 3:2 resonance means the body (Pluto, in this case) completes two orbits of the sun for every 3 orbits that the other body (Neptune, in this case) completes.

bodies outside the orbit of Neptune and seems to define the concept of the Kuiper belt and TNOs. The locations of KBOs, centaurs, comets, and Jupiter's Trojan asteroids are shown.⁶ These are projected onto the plane of the ecliptic. And due to the projection effect and the relatively very large size of the symbols compared to the actual sizes of the objects, the outer solar system appears more crowded than it actually is. Even though the Kuiper belt was proposed independently by Edgeworth in 1949 and Kuiper in 1951, though not as a solution to the problem of short-period comets at that time, there can be no denying it exists.

But could the Kuiper belt have been the supply of short-period comets for the alleged past 4.6 billion years?

From the above analysis, I think it is unsustainable to argue that the KB does not exist. In 2003 there were only 651 KBOs identified, and it was argued that they are not KBOs but TNOs, and hence there is no Kuiper belt (Newton, 2002, pp. 15–17). The argument hinges on the fact that it was proposed as a solution to short-period comets and that the observed bodies are too large to be cometary cores. You can call them all TNOs, but they are located in the region that Kuiper and Edgeworth suggested, and hence they are KBOs.

Whether or not there is a sufficient supply of cometary material there, is another question. But it is fair to note the following:

- The period of time mankind has been observing this region with very good telescopes has been extremely brief.

⁶ Trojan asteroids (also called Trojans) are a large group of asteroids that share the orbit of Jupiter around the sun. Jupiter Trojans are distributed in two elongated, curved regions around the two stable Lagrangian points lying 60° ahead of the planet in its orbit, and 60° behind.

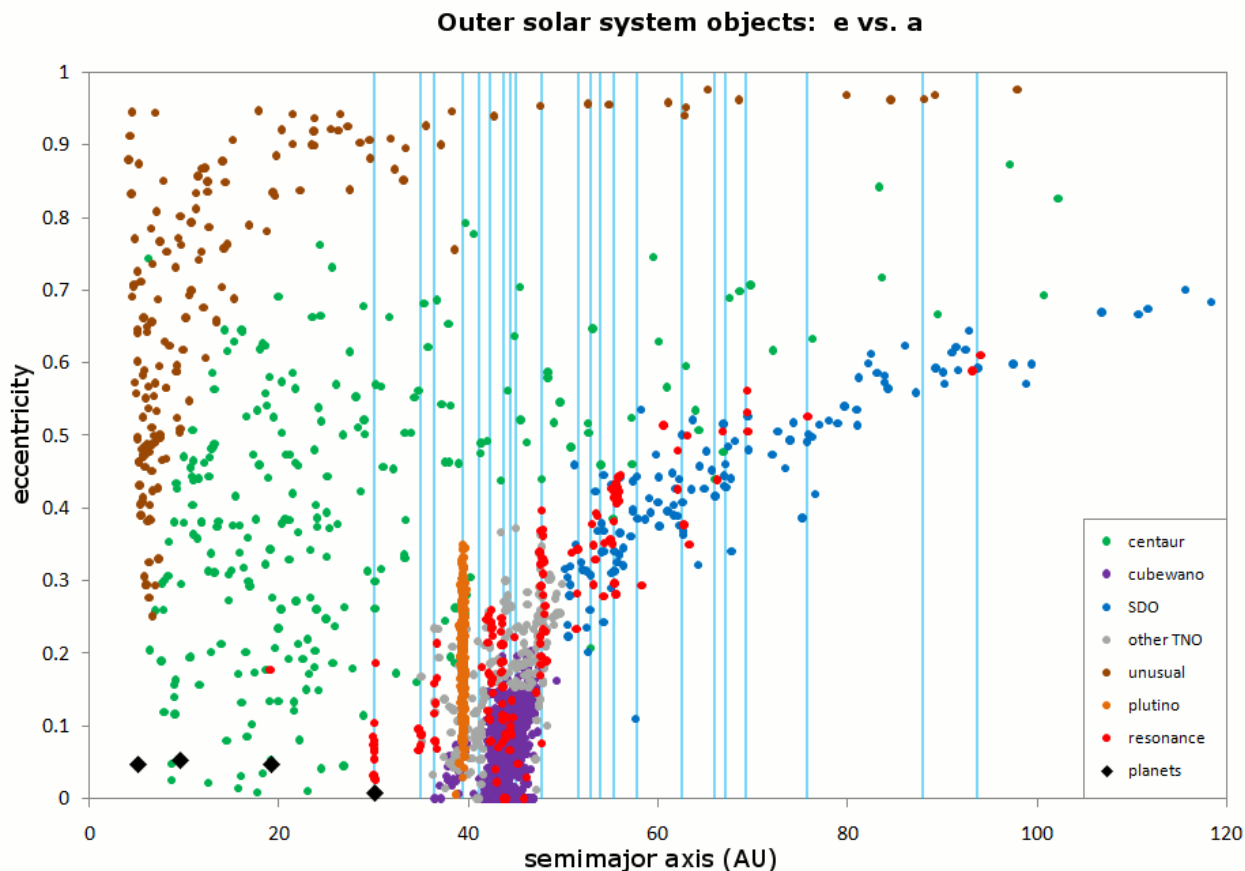


Figure 6. Plot of the eccentricity versus semimajor axis for outer solar system objects (Johnston, 2015c). Red (color in online version found at creationresearch.org) points indicate orbital resonances with Neptune as identified by vertical lines (light-blue, color online). The planets are shown by black diamonds. Neptune is at 30 AU. Beyond 40 AU (Pluto) is a large group of TNOs (purple dots, color online) called cubewano, which is a name for a classical KBO.

- The ability to detect 5 to 10 km-sized objects at 50 to 100 A.U. (see Figure 8) may be extremely poor; hence making an unbiased budget estimate is extremely problematic.
- There are needed on the order of 1 billion cometary cores to maintain a supply for the 4.6-billion-year uniformitarian timescale, which means only about 1000 are needed on a 6000-year timescale.

A comet has the mass of $10^{-10} M_{\oplus}$ (Earth masses), and early solar system formation theory has that there was about 1 Earth mass of material out there initially. Some argue for a much higher mass of $100 M_{\oplus}$ in the Oort

cloud. So even if it was $0.1 M_{\oplus}$ initially in cometary core material, that gives the evolutionists 1 billion comet cores at their origin.

Certainly the existence of about 2000 known KBOs now is consistent with only about 3000 cometary cores at Creation, assuming the smaller cometary cores had a similar abundance to the large KBOs that have been observed. But if there were 1 billion there 4.6 billion years ago, at the observed rate of loss in the solar system, it is possible to have reduced that to only a matter of thousands today. Of course a mechanism is needed to eject the comet cores out of stable orbits in the KB over those

billions of years. The suggestion is that the comets mostly dove into the sun. A total mass of $0.1 M_{\oplus}$ would have had negligible effect on the sun.

Based on the nebular hypothesis and the idea that the Oort cloud resulted from the formation of the solar system, it would be reasonable to say that astronomers regard the KB as an initial reservoir of cometary material that led to the formation of the alleged Oort cloud over the alleged 4.6 billion years.

The comets in the Oort cloud probably did not form at their present locations. Instead, they may be ancient planetesimals that coalesced near the ecliptic in the vicinity

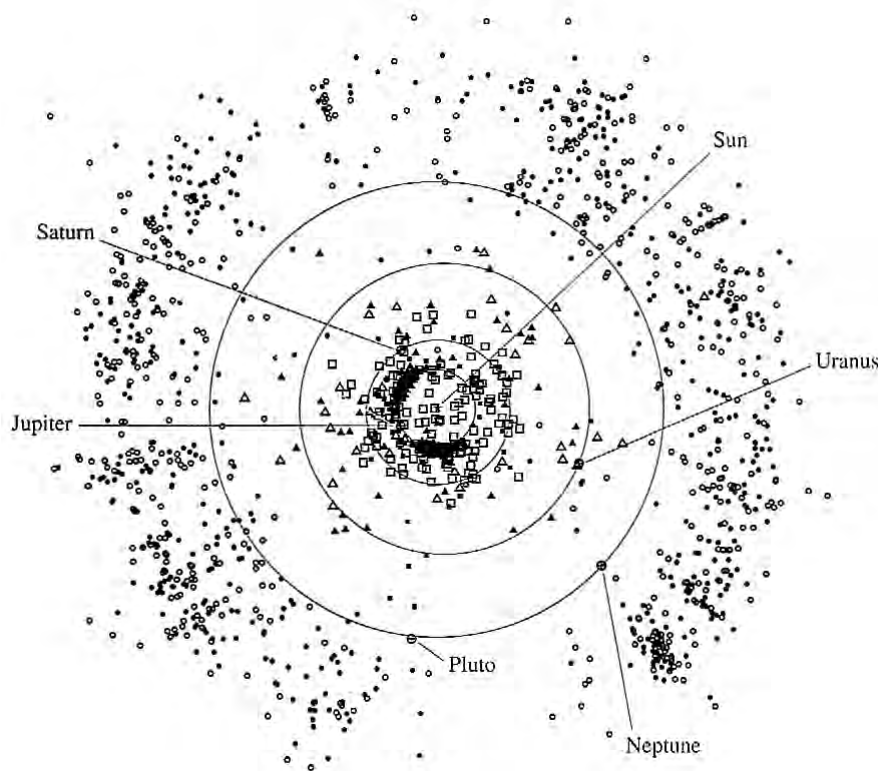


Figure 7. The positions of known classical and resonant KBOs (circles), centaurs and scattered KBOs (triangles), comets (squares), and Trojan asteroids from the orbit of Jupiter outward (two dark patches) as on September 8, 2005. Open symbols are objects observed at only one opposition; filled symbols are objects that have been observed at multiple oppositions. For the comets, the filled squares represent numbered periodic comets; other comets are indicated by open squares. The classical Kuiper belt is clearly evident beyond the orbit of Neptune. In this orientation, the planets and most of the other objects orbit counterclockwise. Excerpted from Carroll and Ostlie (2007, p. 829).

of Uranus and Neptune. After repeated gravitational interactions with the ice giants, the nuclei were catapulted out to their current distances. Because these nuclei were so far from the Sun, passing stars and gas clouds ultimately randomized their orbits, resulting in the nearly spherical distribution that exists in the outer cloud today. With the inner cloud being deeper in the Sun's gravitational well, these cometary nuclei did not become quite as randomly distributed. Therefore,

comets in the inner Oort cloud were able to retain some history of their original locations when the Solar System was young. It is probably the gravitational perturbations of other stars and gas clouds that cause some of the cometary nuclei to start their long falls into the inner Solar System. (Carroll and Ostlie, 2007, p. 826)

Of course this is more storytelling. From the available data, it is now clear that most of the long-period comets have a broad range of inclinations to the plane

of the orbit of the planets—the ecliptic. KBOs are confined near the plane of the ecliptic, so they are unlikely the source of the long-period comets. That leaves only the hypothetical spherical Oort cloud as their main supply. That still has not been observed. There is the claim that there are observed inner Oort-cloud objects (Johnston, 2015d)—objects orbiting beyond the classical Kuiper belt, with perihelia greater than 55 AU. But that seems to be more special pleading than anything else. The minor planet Sedna has a very wide orbit, but that is still within the region of space given to the KB, not the inner Oort cloud, which is supposed to start at 3000 AU.

Conclusion

Observations of comets, the Kuiper belt, and the Oort cloud are consistent with a 6000-year-old solar system, in terms of both short-period and long-period comets. The orbital inclinations of most short-period comets is low, so it may be a straw man to rule out the KB as a source of short-period comets for the uniformitarian theory. It depends critically on the existence of cometary nuclei in the KB, which so far have not been observed in any numbers (Johnston, 2015b). The orbit inclinations of long-period comets is distributed through all inclinations, forming a spherical distribution around the sun. Therefore, the KB cannot be their source, but rather the Oort cloud is needed.

Therefore, the existence of the Kuiper belt no longer is in doubt, and given that most TNO objects are in stable orbits, it is erroneous to say it does not exist. Of course that does not necessarily guarantee a supply of short-period comets over billions of years. There are other problems as well; many binary TNOs have been discovered, for example (Johnston, 2015b). The short-period-comet argument may not be a good young-solar-system argument to make. Since the KB cannot be the source of

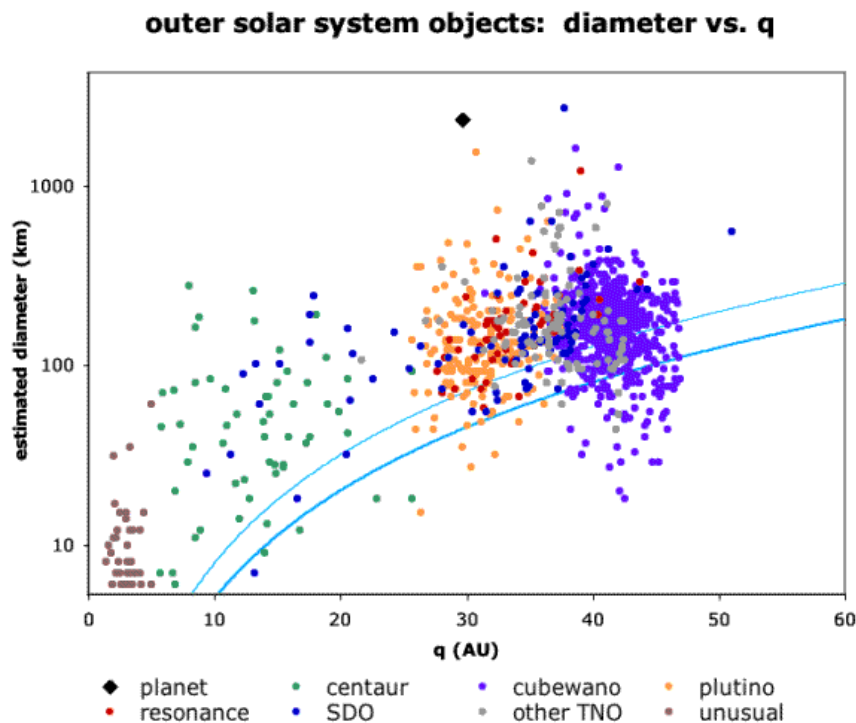


Figure 8. Estimated diameter as a function of perihelion distance (q) for TNOs. Black diamond at 30 AU represents Neptune. A line indicates the nature of the cutoff that would result from detectability limits; in other words, objects lying along this line would have the same apparent brightness from Earth (assuming the same albedo). Note the lack of detected objects with perihelia beyond 47 AU. Reproduced from Johnston (2015d).

long-period comets, the invisible Oort cloud is still needed as the final supply reservoir. However, its existence remains hypothetical.

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Neutron Stars in Globular Clusters: Evidence of Young Age?

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Abstract

The age of globular clusters and the stars they contain is thought to be on the order of 10 billion years. Neutron stars are believed to form via supernova explosions of massive stars, and their progenitor stars have very short evolutionary lifetimes, so neutron star production in globular clusters ought to have ceased billions of years ago. Neutron stars move at high velocities, which are probably the result of large kicks they receive during their formation. Their speeds are more than sufficient for neutron stars to escape from globular clusters within thousands of years. Hence, globular clusters should contain few, if any, neutron stars. Yet, globular clusters typically contain many neutron stars. This suggests that globular clusters may be much younger than generally thought.

Introduction

Globular clusters are centrally condensed, radially symmetric, tightly bound star clusters, containing between 50,000 and a million stars. Astronomers consider globular clusters to be some of the oldest structures in the galaxy, with an average age estimate of more than 10 billion years (Vandenberg, 2013). Recently, Meissner and Weiss (2006) estimated the ages of 46 globular clusters, with ages ranging 8–16 billion years. According to current understanding, the stars in globular clusters share in this age. These age estimates come from the com-

parison of observed color-magnitude diagrams with theoretical Hertzsprung-Russell diagrams (for a discussion of this technique in the creation literature, see Faulkner and DeYoung, 1991). It is believed that star formation ceased early in the history of globular clusters, so that virtually no star formation has happened since shortly after the formation of the clusters.

Neutron stars are very small, but very dense, stars primarily composed of neutrons at nuclear density. Neutron stars are thought to be the stellar remnants remaining from the core collapse

of massive stars resulting in either type II, type Ib or type Ic supernovae. Stars rotate and possess magnetic fields, and neutron stars preserve these properties of their progenitor stars. However, as the cores collapse to form neutron stars, conservation of angular momentum requires that neutron stars rotate very quickly. A similar thing happens to the magnetic fields so that neutron stars have intense magnetic fields. Due to their small size, neutron stars are extremely faint in visible light and thus are difficult to detect in optical wavelengths. However, neutron stars emit considerable energy in the radio part of the spectrum. The radiation is powered through the interaction of charged particles with the very rapidly spinning strong magnetic fields carried along by the neutron stars' rotation. Most of the radio power of a neutron star is beamed

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along a path aligned with its magnetic field axis. The magnetic field typically is tilted with respect to the rotation axis, so the neutron star's rapid rotation beam sweeps the beam around. This causes a neutron star's beam to sweep out a cone similar to a searchlight. If we happen to lie near the cone swept out by a particular neutron star, we can detect it by rapidly periodic pulses. However, if we lie sufficiently far from the cone, we do not. We call neutron stars detected this way pulsars. These observations normally are made in the radio part of the spectrum. Obviously, we cannot detect most neutron stars this way, so the number of neutron stars probably is far higher than those that we actually discover as pulsars.

The only other method for detecting neutron stars is when a neutron star is in a close binary system. The strong tidal force of the neutron star can pull matter from its companion onto the neutron star. The in-falling matter is heated to very high temperature, resulting in copious amounts of X-rays. These X-ray binaries can be observed only above Earth's atmosphere, because Earth's atmosphere is completely effective in blocking celestial X-ray sources. For more discussion of neutron stars in the creation literature, see the review of Faulkner (2008). For most of this paper, neutron stars will be discussed in the context of pulsars, so in some respects these terms will be used interchangeably.

High Velocity Neutron Stars

Neutron stars frequently have anomalously high velocities as compared to most stars in the galaxies. Neutron star velocities typically are on the order of hundreds of km/s or even thousands of km/s. This was first noted by Gunn and Ostriker (1970) on the basis of the higher dispersion of pulsar locations above the galactic plane as compared to O and B type stars, the presumed progenitors of neutron stars. The high

velocities have been confirmed by later studies using the same approach but much more data that has been gathered. Additionally, many pulsars have now had their proper motions measured with radio telescopes, offering more direct evidence of the common high velocities of pulsars. Proper motions can be converted to tangential velocities, provided that we know the distances to the pulsars in question. Fortunately, distances of pulsars are relatively straightforward to measure by taking advantage of dispersion. Dispersion refers to a slight time difference in the arrival of pulses at various radio frequencies. Dispersion depends upon the frequencies used and the column density of free electrons in the intervening interstellar medium (ISM). We have a good understanding of the density of free electrons in the ISM, so observed dispersions can be converted to distances.

However, tangential motion is only one component of space motion, the other component being radial velocity. Radial velocities are much more difficult to determine for pulsars, so many studies find only tangential motion. Therefore, actual space motion would be greater than simple tangential motion. In statistical studies of a large number of pulsars, the average space motion would be the square root of 2 greater than the average tangential velocity.

The study by Cordes and Chernoff (1998) produced space velocities for 49 pulsars. Table 1 reproduces their results. The average speed is 384 kilometers per second. The minimum speed is 162 kilometers per second. These results are conservative, for other studies have suggested higher averages. For instance, Zou et al. (2005) published tangential velocities of 74 pulsars. The average tangential velocity was over 1,000 km/s. However, if radial velocities were included, the space velocities would be even larger. Hobbs et al. (2005) reevaluated motions of 233 pulsars, in which they concluded that young pulsars have a

mean velocity of 400 km/s, though some have velocities of over 1,000 km/s. The situation recently has been summarized by Wongwathanarat, Janka, and Müller (2010):

Young neutron stars (NSs) possess average space velocities around 400 km/sec, much larger than those of their progenitor stars, implying that they are accelerated during the birth in a supernova (SN) explosion.

In addition, there may be a selection effect against detecting the higher speed pulsars, because they likely have moved far from our location near the galactic plane or might even have escaped the galaxy. At such great distance from us, it is difficult to measure their proper motions. Hence, the true average neutron star velocity may be greater than measured.

There have been several proposed explanations for the prevalence of pulsars having high velocity. The most common explanation is asymmetries in the supernova explosions that formed the neutron stars. An asymmetry in a supernova explosion would impart a kick to the forming neutron star via Newton's third law of motion. Hence, astronomers call the high velocities of neutron stars kick speeds, or simply kicks. Lai (2000) has reviewed the various proposed mechanisms for neutron star kicks.

Neutron Stars in Globular Clusters

In recent years, it has become apparent that pulsars (and hence neutron stars) are common in globular star clusters. For instance, the recent catalogue of Freire (2012) lists 144 pulsars in 28 globular clusters. While conducting a deep Chandra X-ray satellite survey of the globular cluster 47 Tucanae, Heinke et al. (2005) estimated that the cluster contained at least 300 neutron stars. Note that this result was based upon the number of X-ray binaries that the authors thought that they detected.

Though it is difficult to measure directly the speeds of pulsars in globular clusters, globular cluster neutron stars would have to be fundamentally different from field neutron stars (neutron stars that do not appear to be part of a cluster) for them not to have kicks as well. Assuming that they have similar kicks as field neutron stars, neutron stars in globular clusters ought to exit their hosts within thousands of years, not millions or billions of years.

Astronomers are confident that neutron stars represent an end state of massive stars. But massive stars have short lifetimes, on the order of tens of millions of years, far shorter than the billions of years generally assumed for globular clusters. Therefore, no neutron stars should have formed in galactic globular clusters for billions of years. So why are there still neutron stars in globular clusters? A recent article admits this is a problem that secular astronomers need to resolve:

There is mounting evidence that as many as 1000 neutron stars (NSs) may be present in some of the richest globular clusters in the Galaxy, which perhaps amounts to more than 10%–20% of the NSs ever formed in each cluster. Such a large NS retention fraction is seemingly at odds with recent estimates of the characteristic “kick” speeds of single radio pulsars in the Galaxy, ranging from roughly 5 to 10 times the central escape speeds of the most massive globular clusters. This retention problem is a long-standing mystery. (Pfahl, Rappaport, and Podsiadlowski, 2002, p. 283)

Or consider the words of Kuranov and Postnov (2006, p. 394):

The hypothesis of high space velocities of young NSs immediately leads to the well-known problem of NS retention in GCs, since the escape velocity even in the densest clusters does not exceed several tens of km/sec. Most of the NSs born through

the core collapse of massive stars should have escaped from the cluster shortly after its formation.

Adopting a kick speed typical of neutron stars, we can estimate the time required for a neutron star to escape from the center to the outer edge of a globular cluster. Using somewhat unconventional units, let t be the time of escape in years, c the velocity of light in km/s, v the kick velocity of a neutron star also in km/s, and r the radius of the globular cluster in light years.

$$t = \frac{c}{v} r \quad (1)$$

The energy required to overcome the gravity of a globular cluster would slow the neutron star, and hence increase the time for the neutron star to escape. However, the escape velocities from the cores of globular clusters are on the order of tens of km/s, about an order of magnitude less than a commonly accepted typical kick for neutron stars. Thus, this factor would increase the required escape time only marginally.

Using the above formula, I computed the escape time for neutron stars for the 29 globular clusters in the Messier Catalogue. The physical sizes of the globular clusters were taken from various sources in the literature. The results are tabulated in Table 1. I computed two escape times. The faster escape times assume a kick speed of 450 km/s, a commonly accepted value, while the slower escape times assume a much more modest kick speed of 100 km/s. Even using the slowest speed, the maximum age is only 660,000 years. Again, consideration of overcoming the gravitational binding of a kicked neutron star originating near a globular cluster's core would increase these escape time estimates only marginally. This sample represents about 20% of the total number of galactic globular clusters. These are the brightest globular clusters (a result of being among the closer globular clusters to

us) visible from temperate latitudes of the Northern Hemisphere. However, astronomers believe that the Messier Catalogue globular clusters represent a good sample. Since the neutron star formation rate within globular clusters is assumed to have been zero for billions of years, how can there still be neutron stars within globular clusters?

Since this has been a long-standing problem for the currently understood theory of stellar evolution, it is not surprising that astronomers have addressed this issue. In their estimation, the most promising solution to the problem is to appeal to neutron stars existing in close binaries. When two stars are in close proximity as they are in close binaries, the two stars affect each other's development. Indeed, binarity appears to be implicated in a host of astrophysical processes, such as all types of novae and some types of supernovae. They are implicated in millisecond pulsars (MSPs) as well. Millisecond pulsars have rotational periods on the order of a millisecond. It is believed that some pulsars may be created with millisecond periods. However, the radiation that pulsars emit is powered by rotational kinetic energy. As pulsars age, their rotation periods decrease. The age of a pulsar can be estimated by the spin-down rate, the age given by $P/(dP/dt)$. Hence pulsars, regardless of their initial periods, rapidly increase their periods far out of the millisecond range. Why are there so many millisecond pulsars? In close binary stars, matter and angular momentum transfers from one star to its companion. In this manner, millisecond pulsars have been spun up from the original longer periods. These rejuvenated millisecond pulsars sometimes are called recycled pulsars. There is much observational evidence to support this understanding. A close companion can reduce the kick that a forming neutron star receives by absorbing some of the kick. There is observational evidence of this. Toscano, et al. (1999) presented velocities of 23

Globular Clusters Name	Low Kick Max Age Years	Average Kick Max Age Years	Cluster Radius Light Years	Secular Age Years
Messier 2	261,900	58,200	87	13 billion
Messier 3	270,000	60,000	90	8 billion
Messier 4	105,000	23,333	35	12.2 billion
Messier 5	240,000	53,333	80	13 billion
Messier 9	135,000	30,000	45	12 billion
Messier 10	124,800	27,733	41.6	11.39 billion
Messier 12	111,600	24,800	37.2	12.67 billion
Messier 13	252,000	56,000	84	11.65 billion
Messier 14	150,000	33,333	50	14.2 billion
Messier 15	264,000	58,667	88	12 billion
Messier 19	210,000	46,667	70	11.9 billion
Messier 22	150,000	33,333	50	12 billion
Messier 28	90,000	20,000	30	12 billion
Messier 30	279,000	62,000	93	12.93 billion
Messier 53	660,000	146,667	220	12.67 billion
Messier 54	459,000	102,000	153	13 billion
Messier 55	144,000	32,000	48	12.3 billion
Messier 56	126,000	28,000	42	13.7 billion
Messier 62	147,000	32,667	49	11.78 billion
Messier 68	159,000	35,333	53	11.2 billion
Messier 69	126,000	28,000	42	13.06 billion
Messier 70	102,000	22,667	34	12.8 billion
Messier 71	39,000	8,667	13	9.5 billion
Messier 72	126,000	28,000	42	9.5 billion
Messier 75	201,000	44,667	67	9.5 billion
Messier 79	354,000	78,667	118	11.7 billion
Messier 80	144,000	32,000	48	12.54 billion
Messier 92	357,000	79,333	119	14.2 billion
Messier 107	118,500	26,333	39.5	13.95 billion

Table 1. Messier Globular Clusters, Escape Times

millisecond pulsars with an average of 85 km/s:

Most of the ordinary pulsars have velocities up to 500 km/sec, with a

small number of pulsars with velocities as high as 1000 km/sec: The vast majority of MSPs, however, have velocities less than 130 km/sec and

average just 85 km/sec $\pm$ 13 km/sec. (Toscano, et al, 1999, p. 929).

However, even these lower velocities are more than adequate to overcome the gravity of globular clusters, because the average core escape velocity for globular clusters is at most 50 km/s. All this would succeed in doing would be to retain the few MSPs on the extreme low-energy tail of the distribution and slightly lengthen the escape time of the others.

Since the typical lower kick speeds of binary neutron stars is insufficient to solve the neutron star retention problem for globular clusters, another proposed solution is that there is a bi-modal distribution of velocities with one mode having essentially zero kick velocity. For instance, Podsiadlowski et al. (2004, p. 1044) observed:

Further observational evidence that at least some NSs receive low kicks at birth is provided by the fact that a large number of NSs are found in globular clusters; some massive globular clusters may contain more than 1000 NSs. Since the central escape velocity is generally 50 km/sec, essentially all of the NSs born in a globular cluster should escape from the cluster if they received a kick consistent with the kick distribution for single radio pulsars.

Notice that they have converted the problem into “evidence” (their term) for the solution to the problem! As of yet, there is no clear empirical evidence that there is bimodal distribution in neutron star velocities.

Conclusion

The high velocity nature of neutron stars is well established. It also is a well-established fact that globular clusters contain a significant number of neutron stars. These conclusions are based upon empirical data collected in recent decades. It is the consensus position that globular clusters and the stars that they contain are very old. However, this is a matter

of interpretation of data based upon evolutionary assumptions. There are no theoretical or observational reasons why neutron stars within globular clusters are fundamentally different from field neutron stars. Therefore, neutron stars within globular clusters probably have high velocities as well. These velocities are sufficient for the neutron stars to have escaped from the globular clusters in thousands of years. Hence, the large number of neutron stars in globular clusters is a dilemma for the evolutionary worldview. The existence of so many neutron stars in globular clusters may be evidence of recent creation.

How do biblical creationists explain high velocity neutron stars? That is not clear. There are reasons to accept the usual explanation of neutron stars as the result of certain supernova explosions (Faulkner, 2008), but perhaps at least some neutron stars might have alternate explanations. Did God create some neutron stars at the beginning? If so, did He make them with high velocities? If so, why? In a recent creation, might we expect fewer supernovae in the history of globular clusters than in the evolutionary model and hence fewer neutron stars in globular clusters today? Unfortunately, these answers await a more fully developed creation theory of astronomy.

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Cells as Information Processors

Part 2: Hardware Implementation

Dr. Royal Truman*

Abstract

Cells use many codes, which operate through abstract symbolism and formal rules. To instantiate the logic, dedicated decoding processors—hardware molecular machines—must interpret each kind of variable and the associated values. Decoders include ribosomes, DNA polymerases, RNA polymerases, spliceosomes, Hsp70 and Hsp60 chaperones, proteasomes, RNA degradasomes, protein translocases, reverse transcriptases, aminoacyl-tRNA synthetases, and error-correcting machines.

Many codes are mutually dependent in order to function, and cells could not have evolved each decoder sequentially. Ribosomes require the mRNAs from DNA-dependent RNA polymerases, but these polymerases are composed of protein products from ribosomes. Both decoders require the energetic ATP molecules from ATP synthases, which themselves cannot exist until ribosomes and RNA polymerases already work. Being coded information systems, additional guidance is provided in cells through engineered components such as the cytoskeleton, lipid rafts, membranes, pores, chemical gradients, correct placements of synapses, correct binding strengths, and nuclear subcompartments.

Computer architectures structure long-term storage capacity hierarchically to process data at different levels of granularity: data centers and distributed file systems; hard discs; disk partitions; files and extents; tracks; sectors and data blocks; and bits. In cells the same kinds of hardware principles are observed: ecologies of cooperating bacteria and multiple cells in eukaryote organisms; genomes; chromosomes, plasmids, mitochondria, and chloroplasts; euchromatin/heterochromatin and DNA looping; DNA regions defining primary RNA transcripts; exons/introns; and nucleotides.

Cells must be interpreted as holistic systems whose origin cannot be explained by neo-Darwinian theory.

Introduction

In Part 1 (Truman, 2016) of this two-part series, we showed that formal data struc-

tures, generic programming constructs, and file formatting are used in both computer programming and cells to process

logic. Many independent codes exist in cells, each developed from elementary symbols and used by their own programs. These codes rely on variables and values and, reminiscent of computers, have well-defined data types and a list of valid operations that can be performed

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with them. In both cells and computers, variables or fields can be used to create indices and concatenated indices (for example cis-regulatory elements) to identify the location of data (the portion of DNA to transcribe).

Data values can be assigned to variables (such as when a receptor is suitably bound by a ligand) and stored in linked lists (as seen in data processing by RNA and DNA polymerases) and arrays (for example translation of mRNA codons). The location of data also can be identified by “pointers” to memory addresses (as occurs in cellular signaling cascades). The various programs consist of formal software elements such as Boolean logic; iteration with clearly specified start and termination rules; control structures such as “GoTo,” “wait,” and processing commands permitted for that data type. Computers and cells also implement short- and long-term data storage, parallel processing, source code sharing and reuse, data compression, and data archival.

These software elements permit intended outcomes to be specified using formal symbolic logic. Abstract variables

can be manipulated; for example: if $x=\text{true}$ and $y=2$ then {do the following}. The stepwise instructions can be defined without considering the physical implementation.

Here in Part 2 we now consider how the cellular programs get instantiated, showing once more that there are remarkable parallels with how data is physically organized and used by computers. We will emphasize the need for very complex cellular hardware to process the different codes and how these are part of the holistic design of adaptable, self-correcting, and self-replicating cells.

Distribution and Partitioning of Available Storage Capacity

Data Storage Formatted Hierarchically

Significant advantages result from creating architectures to structure how data is stored physically. These structures are transparent to the processing logic but can affect the speed and reliability of execution. Computers and cells use well-defined standards to store data in

a hierarchical manner, with each level including one or more members of the subordinate level (Figure 1). Although the analogies suggested in Figure 1 display remarkable similarities between computer and cellular technologies, they should be viewed as illustrative only. Computer technologies could change in the future, and not all cell types are identical (e.g., prokaryotes/eukaryotes). In the computer-versus-cellular analogies, some of the layers operate independently. The location of database data blocks is independent of physical sectors, and parts of exons could be located within a single nucleosome (and vice versa). In all cases, there are good design reasons for organizing parts of the data in specific manners, and special read/write technology is necessary for all layers of the architecture.

Data centers and distributed file system

Different and multiple copies of computer data are often stored separately, on disc arrays, separate servers, and data centers. In an analogous manner, ecologies of bacteria store both different data and multiple copies of the same genome. Higher eukaryotes also store different data in separate organisms and multiple copies in different cells within the same organism. By cellular data we are not limiting ourselves to DNA. In Part 1 (Truman, 2016) of this series, we pointed out that coded variables and values are stored on DNA, RNA, proteins, sugars, membranes, and other biochemical substances.

Hard disc

It often makes sense to organize essential data in one easily accessible location. Storage media such as hard discs are used by computers linked to hardware processors and external devices. In the case of cells, such data are also placed together within the organism and linked to data processors, everything within a protective membrane to separate from the environment.

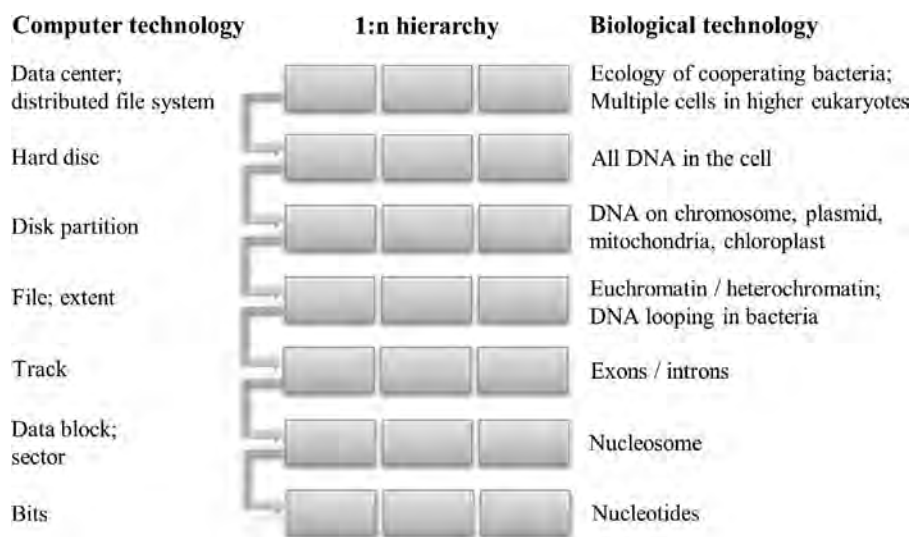


Figure 1. Computers and cells organize storage capacity hierarchically, with each level containing multiple members of the embedded sublevel.

Disk partition

Long-term storage capacity for computers is often separated into partitions, which act as separate disk drives. Data can often be transferred between partitions, and sometimes they contain different operating systems or types of data. This is also true of cells, which organize the available DNA into separate chromosomes, plasmids, mitochondria, and chloroplasts. Partitioning must be unambiguous. This is implemented in plasmids by making them circular. Initiation of chromosome replication in prokaryotes is defined by sites called *origins of replications* and a special *terminus* regions identity where replication terminates. In eukaryotes, chromosome initiation sites called *autonomous replication sequences* (Shapiro, 2011, p. 36), along with centromeres (O'Sullivan and Karlseder, 2010; Sullivan et al., 2001) and telomeres (the caps at the ends of chromosomes) (Sadaie et al., 2003) identify individual chromosomes.

File, Extent

A disk partition can contain many files, or database extents. Similarly, chromosomes in eukaryotes are organized into smaller portions called euchromatin and heterochromatin (Shapiro and von Sternberg, 2005; Shapiro 2006). A computer file may contain records of varying lengths (e.g., in databases), even as sections of DNA euchromatin can contain multiple transcription regions. In bacteria, a similar principle is performed using DNA loops created through bound proteins, which lead to physical segmentation of the DNA (Cournac and Plumbridge, 2013).

Track

A track forms a circle on the hard drive platter and represents only a small portion of the entire data on the hard disk. In a comparable manner, introns and exons are also subdivisions of transcription regions.

Sector and data block

Sectors and database data blocks typically contain a fixed number of bits. A database extent can contain several blocks, and a track contains several data sectors. In eukaryotes nucleosomes also represent small, fixed-length data storage units within transcription regions.

Bits

The smallest entity used digital computers are bits, and for DNA this corresponds to nucleotides.

External devices

In addition to structuring data hierarchically, electronic data can be stored on external devices such as printers, scanners, and cameras. Cells can also interact with DNA stored externally, such as on viruses and microRNA's in vesicles travelling the blood system. Furthermore, DNA on bacteria associated with higher organisms provide them with many valuable functions.

Design Reasons for Structuring Storage

Process data at different levels of granularity

For different purposes, such as storage, retrieval, and processing, the data sometimes involves large amounts of undifferentiated data and other times specific structured data. If a hard disc is badly corrupted and the damaged part cannot be repaired, then the entire content must be replaced. But sometimes an identifiable subset only was read or written incorrectly—such as a partition or data block, or IP packet—and the correction should be executed at the correct level of granularity. In a similar manner, a severely damaged organism (“data center”) may need to be replaced, or only a damaged single cell, or an alternative plasmid copy should be used, or only sections of mismatched DNA strands.

Concurrent access

Permitting concurrent access to different data removes processing bottlenecks, which requires that relevant subportions of the data be demarcated. Multiple RNA polymerases can transcribe simultaneously on the same or different chromosomes, different ribosomes can translate different (and sometimes the same) mRNA, and cells can work independently of each other.

Local and distributed processing

Sometimes processors need to be moved to where data can be collected, as in process controllers linked to manufacturing sensors. Analogously, bacteria with their data processing equipment need to be located near nutrients.

Other times data needs to be transferred to where it can be processed, as in computer client server architectures. In cells, various genes required for a specific function are often brought together for processing in transcription factories (Mitchell and Fraser, 2008; Melnik et al., 2011).

Process different kinds of data on different physical media

Structuring data correctly, including file-type formatting discussed in Part 1, permits specialized software to process raw data for images, sounds, spreadsheets, and so on effectively. In an analogous manner, different codes in cells require that DNA, RNA, protein, and other media be physically prepared properly to permit data to be stored and retrieved from them. In this paper, we limit detailed analysis to how DNA and RNA are organized to optimize logic processing by difference programs. Future work will reveal how other information carriers are structured, such as for proteins (motifs, domains, multi-domain complexes, etc.).

Effective interaction between long- and short-term memory and backup copies

Instead of loading terabytes of irrelevant content from a hard disk into short-term

memory, it makes more sense for an application such as a database query to read a limited number of relevant blocks into memory. It is also more efficient to read only once a large amount of data that includes a substructure of relevant parts. Recreating the transcription apparatus (ribosomes) for each individual protein needed is less efficient than to activate multiple relevant genes concurrently, as done by operons and transcription factories (Rieder et al., 2012).

Available memory in computers and cells can be reorganized and freed up for other purposes. RNA no longer needed is degraded to free up “short-term memory” and re-created when needed from only small portions of chromosomes.

Cellular Hardware Plays Multiple Roles

The software constructs discussed in Part I are used to express processing needs, independent of the hardware. But at some point, a physical implementation is necessary to be of any use. Computers require many hardware components to work, and not only processors, to interpret the coded data. Electrical power is delivered via cables to the correct location, temperature needs to be regulated, and sensitive parts protected from the environment.

Physical structures in cells must also provide many services, in addition to interpreting the codes. Hardware such as membranes, pores, and protein filaments can channel outcomes to produce the intended results, which is a feature of coded information systems (Truman 2012a, 2012b, 2012c 2012d, 2013, 2015). This guidance, like the effect from coded messages, decreases the entropies with respect to a reference state. Hardware components in cells, however, must do far more than in computers. Cellular hardware must be adaptable and dynamic with respect to when and where they are made avail-

able, how long they exist, and even the number of processor copies.

Hard and Software Independence in Digital Computers

Since the seminal Turing machine model created by British mathematician Alan Turing (1912–1954), hardware engineers can work largely independently from software programmers. In Turing machines, symbols are stored on a readable tape using a simple head reader and a small rule set. Modern digital computers are generally based on the more refined Von Neumann or the Harvard architecture, using stored programs with instructions, processed by separate hardware that performs the calculations (Bray, 2009, p. 40).

No human computer technology can match the sophistication of cells, which self-repair, replicate autonomously, and manufacture most of the components needed (including their own energy supply). Cellular decoders process the variables and values used by the different codes found on DNA, RNA, proteins, and sugar, as discussed in Part I. But cells can do many things no computer system can match. They can regulate when, where, and how many processors (for example DNA polymerases, tRNAs and ribosomes) are concurrently in use. This can depend on a developmental schedule, be a response to current biological needs, and be affected by external signals.

The Turing (Turing, 1950), von Neumann, and Harvard computer models provide a partial picture for how cells process logic, being unable to take into account the direct physical participation of the genome in reproductive and regulatory interactions (Shapiro, 2013, p. 289). These models do not naturally capture the cellular reality of multiple codes, often overlapping the same physical location and requiring many kinds of integrated decoding processors. Nevertheless, at a fundamental level cellular codes are being processed as

part of a complex program with high fidelity, and the insights gained from digital and analog computers are useful to understand why cells are not simple mechanical machines. We will distinguish next between cellular hardware which process coded parameters from hardware that do not use a code to guide their operations.

I. Hardware Processors Necessary to Decode

In Part I (Truman, 2016) we discussed how variables are restricted to data types, such as integer, alpha numeric, and Boolean for computers, and that many data types are used in cells, constructed from elementary symbols having definite electronic and geometric characteristics.

A key to understanding cells is to recognize that different codes are used to establish linked chains of sending and receiving variable values. Each code uses variables that can assume values. One region of a ribosome defines a variable that can assume one of 65 values (a codon or be empty). A different region of the same ribosome defines a variable able to assume the value of one of 20 amino acids on the growing chain. RNA nucleotides can also be used to define variables, such as in the intron/exon splicing and other codes.

Each cellular code requires its own kind of decoder. Ribosomes cannot work with splicing signals recognized by spliceosome, nor can spliceosomes work on the basis of codons.

The principle becomes apparent. Cis-regulatory element binding sites (CREs), protein phosphorylation sites, methylated DNA, hormone receptors, mRNA sites recognized by miRNAs, etc. each use their own distinct variables. These codes can only be processed using their own unique decoding hardware machinery, the variables possess a unique data type, and they are limited to a set of allowed operations.

Data Structures Require Precise Engineered Components

In Part I, we discussed the need for software logic to express intentions correctly, and we now discuss the decoding hardware also necessary for the informational system to work. The molecular machines involved must be able to do the right (and avoid doing the wrong) thing for all the codes used in cells. For example, in eukaryotes spliceosomes must identify precisely the nucleotide ends that define the intron/exon boundaries to create up to thousands of possible protein variants, as in the case of neurexin genes in nerve cells or the protein Dscam (Bray, 2009, p.158). Rampant false positives would be deadly.

Molecular machines require very low amounts of energy (Mavroidis et al., 2004) and lie at the heart of every significant biological process (Erbas-Cakmak et al., 2015; Alberts, 1998; Glogocka et al., 2015). Cells are not a bag of enzymes and biochemical reactants but regulated systems working on individual molecules (Glogocka et al., 2015 p. 248). This contrasts with chemistry as performed by humans:

In stark contrast to biology, none of mankind's fantastic myriad of present-day technologies exploit controlled molecular-level motion in any way at all: every catalyst, every material, every polymer, every pharmaceutical, and every reagent all function through their static or equilibrium dynamic properties. (Erbas-Cakmak et al., 2015 p. 10157)

Cellular machines have, however, inspired the growing research fields of artificial molecular machines and nanotechnology (Balzani et al., 2000).

Let us consider the engineering challenge. For a future (evolving) spliceosome, virtually any nucleotide sequence pattern could be “chosen”—of practically any length—to define the intron/exon boundaries (and the recognition pattern need not be limited to contiguous nucleotides). Therefore, there are

vastly more wrong candidates where a developing spliceosome could tear up DNA strands than a correct pattern that by astonishing good luck happens to delimit useful exons throughout the genome to produce valuable proteins (as individual or multiple exons). An average-size exon is only about 137 nucleotides long, surrounded by a sea of large introns in the pre-mRNA (Berget, 1995; Ward and Cooper, 2010). An indiscriminant evolving spliceosome would almost always produce only interfering mRNAs, at great cost of energy and material.

The same considerations apply to the other cellular decoders, such as DNA and RNA polymerases. Let us consider translation. Nature can have no foreknowledge how to process mRNA or how to develop the genetic code. Nucleotides are chemically complex, and every portion has the potential to interact physico-chemically with other substances.

Suppose that after countless evolutionary attempts a proto-ribosome evolved able to translate all the codons correctly with probability of 0.5 (or incorrectly but with neutral effects) an incredible feat considering there are 20 different amino acids. This would be some point during a Darwinian process of optimization. Assuming a small protein size of 200 residues, binomial probability calculations done with Microsoft Excel reveal that less than two mRNAs out of a million ($p=1.8 \times 10^{-6}$) would have 2/3 or more of the 200 codons (i.e., 133/200 or more amino acids) translated correctly or acceptably (Figure 2). The cell would not be viable even using such optimistic assumptions. A minimum cell requires many, many copies of hundreds of different kinds of functional proteins and no cell lineage could survive such chaos.

We conclude that from the very beginning any ribosome must display astonishing fidelity. The implausibility of evolving hopelessly deficient codes can be applied to many other examples,

such as to specify what part of DNA should be transcribed to produce mRNA and when; and successfully distributing only one member of each chromosomes to daughter cells.

Examples of Some Processors

Having concluded decoders must be very precise *ab initio* to offer any benefit, we will now draw attention to how complex these molecular machines are, using some examples.

Spliceosomes

The spliceosome ribonucleoprotein machine consists of about 300 distinct proteins and five RNAs (Nilsen, 2003; Chen and Moore, 2014; Matera and Wang, 2014; Ward and Cooper, 2010). It is believed the spliceosomes are constructed *de novo* for each round of splicing in an ordered but immensely complex stepwise assembly (Lodish et al., 2000, pp. 413–426). In their review Chen and Moore (2014) refer to “the incredible complexities facing structural biologists bold enough to even contemplate complete structural understanding of the splicing machinery within their lifetimes” (p. 147).

Signals that identify introns on the primary RNA include short sequence motifs at the 5' and 3' splice sites (typically a GU and AG respectively); a branch point sequence that contains an adenosine; and the polypyrimidine tract (Figure 3). A typical mammalian gene has 7–8 exons spread out over ca. 16 kb. The exons are relatively short (~100–200 bp), and the introns >1 kb. A typical processed mRNA consists of ca. 2.2 exons. Trans-splicing occurs when exons from different transcripts are linked, encoding chimeric proteins (Lasda and Blumenthal, 2011; Michaeli, 2011; Frenkel-Morgenstern et al., 2012; Heraï and Yamagishi, 2010).

Ribosomes

Ribosomes, where translation of mRNAs occur, are composed of 54 ribosomal

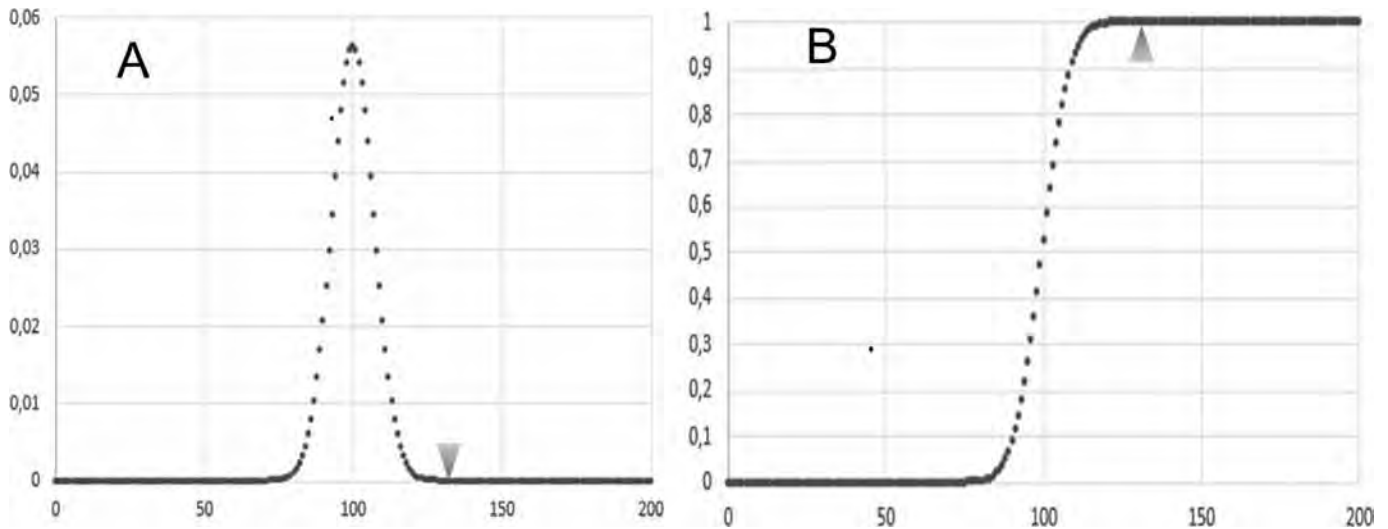


Figure 2. Probabilities for 200 codons to be translated correctly (or wrong but with neutral effects), assuming each codon has an average individual $p=0.5$ of success. From binomial probability statistics, this leads to mean = 100, $\sigma = 7.07$. Arrows show the location of 133 successes.

A: Probability of 0, 1... to 200 successes for the 200 codon attempts.

B: Cumulative probability of success for the 200 codon attempts. For the 200 codons, 52.8% will have between 0 and 100 translated correctly, and 99.9999% will have $\frac{2}{3}$ or less.

During an earlier evolutionary period having an average probability $p=0.1$, over 99.9999999% of a 200-codon mRNAs would have only 0 to 50 codons translated correctly (or wrong but with neutral effects), i.e., one-fourth of the mRNA's codons (mean = 18, $\sigma=4.24$).

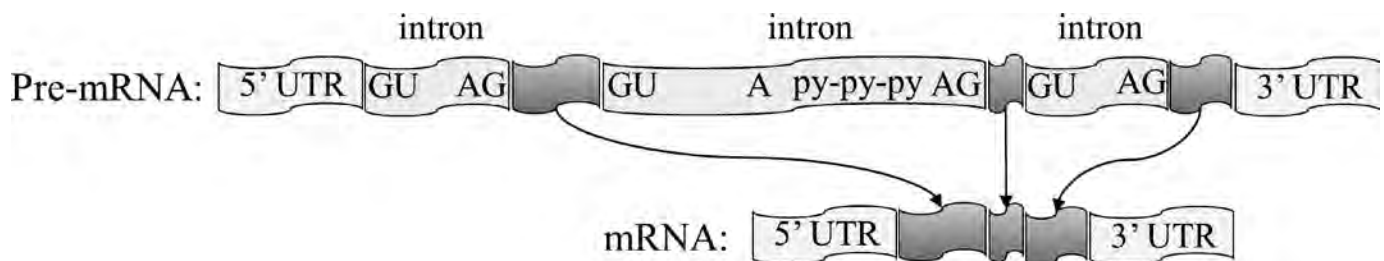


Figure 3. Results after a spliceosome has removed introns. Introns are usually delimited by GU and AG at each end and additional nucleotide patterns near the intron/exon boundary help identify the key di-nucleotides. A key internal A and polypyrimidine tract are also involved.

proteins and 3 large RNA molecules in prokaryotes (Chen and Williamson, 2013; Staley and Woolford, 2009) and 79–80 proteins and four ribosomal RNAs (rRNAs, >5500 nucleotides) in eukaryotes (Wilson and Doudna Cate, 2012).

Ribosomes are worthless until all the multidomain aminoacyl tRNA synthetases (aaRS) are also fully operational in addition to the proteins needed to create these enzymes. We observe that charging the tRNAs requires another, nongenetic code (Trifonov, 2011; Hou, 1988). Twenty different types of aminoacyl tRNA *synthetases* (aaRSs) are found in all organisms, each responsible to covalently link the correct amino acid to the correct tRNA. These aaRS differ in length, three-dimensional structure, molecular weight, and subunit organization, and are very different in amino acid sequence (Panwar and Raghava, 2010).

For translation to work well enough to have any value, a large number of other enzymes are also needed for quality control purposes. These are very precise machines that ensure error rates between 1/2400 to 1/40,000 although the differences between amino acids are miniscule, such as a single methylene group (Nureki et al., 1998; Sarfati, 1999).

Proteasomes

Proteasomes degrade unneeded, damaged, and misfolded proteins in eukaryote cells and some archaebacteria. In eukaryotes, the proteins to degrade are identified by conjugation to ubiquitin proteins (Amm et al., 2014). The eukaryote 26S proteasome consists of 33 distinct subunits (Besche et al., 2009), including the 20S proteolytic core chamber (where protein degradation occurs), which is attached to two 19S regulator caps on each end. These caps consist of about 20 different proteins, which serve to capture and guide proteins into the chamber. 19S caps and ubiquitination have not been found in archaebacteria.

Proteasomes can also interact with the immune system by generating short peptide fragments from pathogens that are used as antigens on the surface of lymphocytes to mount an immune response (Wang and Maldonado, 2006).

DNA Polymerases

DNA polymerases are involved in several key processes, such as DNA replication, many kinds of DNA repairs (Ball et al., 2014), translesion DNA synthesis, DNA recombination, cell cycle control, DNA damage checkpoint functions, and chromatin remodeling (Hübscher et al., 2000; Wu et al., 2014). DNA polymerases are highly accurate, with an intrinsic error rate of less than one mistake for every 10^7 nucleotides added (McCulloch and Kunkel, 2008; Kunkel and Bebenek, 2000).

Most DNA polymerases have a similar three-dimensional fold despite having virtually no sequence similarity (Federley and Romano, 2010). Five kinds of DNA polymerases are known in *E. coli*, 8 in *Saccharomyces cerevisiae*, at least 15 in humans, and 12 in *Arabidopsis thaliana* (Garcia-Diaz and Bebenek, 2007, p. 105), but even DNA polymerases in the same family often display very different properties (Garcia-Diaz and Bebenek, 2007, p. 105).

Some polymerases consist of a single polypeptide chain, and others, such as those involved in chromosome replication, are composed of several subunits. Even the single-chain versions are large and complex. For example, the first DNA polymerase discovered was Pol I, which is ubiquitous in prokaryotes. The *E. coli* version of the enzyme is composed of 928 amino acids (Brown et al., 1982). The processes carried out by polymerases are very demanding. For replication of the two DNA strands, the leading strand is synthesized in the 5' to 3' direction and the other lagging strand in the opposite direction.

Many more proteins are needed that collaborate with these large polymerases.

For replication alone this includes those forming the origin recognition complex (ORC) so the polymerase can access the DNA, the replication protein A (RPA proteins), the MCM complex to unwind DNA, proteins to guide polymerase switching (on the lagging strand polymerase switching is necessary about every 100–200 nucleotides synthesized) and proteins to prevent premature dissociation from the DNA template (Cotterill and Kearsey, 2014).

RNA Polymerases (RNAP)

RNAPs are also very complex. Even bacterial RNA polymerases are very large. The core enzyme requires several proteins and consists of 5 subunits besides a transcription initiation factor sigma (σ) (Ebright, 2000). Using about 110 Daltons per amino acid and a median protein size of 267 for bacteria, the ~400 kDa core enzyme is equivalent to about 14 different proteins working as a unit. Figure 4 shows a strand of RNA being produced. Furthermore, in *E. coli* more than 100 transcription factors have been identified that modify the activity of RNAP (Ishihama, 2000). Multiple types of RNAP are found in eukaryotes (RNA polymerase I–V) (Ebright, 2000). RNA and DNA polymerases are so different that postulating an evolutionary common origin makes no sense.

Unique feature of cellular decoders

A series of papers presented at the 2012 Conference on Engineering and Metaphysics drew attention to the requirements for self-replicators to work (Mignea, 2014). The few examples of complex decoders presented above still fall short of expressing how sophisticated cellular technology is. In computers, the hardware is manufactured once and then reused multiple times to run programs until wear and tear renders it unusable. In cells, hardware processors such as RNA polymerases, spliceosomes, and ribosomes are built, disassembled, and then rebuilt over and over again



Figure 4. RNA polymerase (RNAP) during elongation (from Google Creative Commons, labeled “for commercial reuse with modification”).

and at the location needed. This must be quantitatively regulated according to need and cell type. There are approximately 20 thousand ribosomes in *E. coli*, and up to 10 million in human liver cells (Woodward and Gills, 2012, p. 43). This is a general observation for cells, which regulate when, how many, and where the decoding processors are built, reliably and over thousands of generations.

Optimization trade-offs are at play. Reliably repairing entire molecular machines damaged by bond breakage, oxidation, and other chemical reactions is probably not feasible as a design concept, so rebuilding from high-quality components makes sense. There are also cases where the biological information

processing equipment, once formed, remains intact during the remainder of the organism’s lifetime to constantly process signals, like the whisker neurons of mice, which link through a complex relay path to the cerebral cortex (Kirschner and Gerhart, 2005, p. 161). This also makes sense, since whiskers are important sense organs needed continually to navigate in the dark and tens of thousands of perfect copies are not needed.

Classification of Molecular Machines

The cellular hardware that process the variables and their values in the different codes are examples of molecular machines (MMs). New MMs are being

reported continually (Alberts, 1998; Luskin, 2010), and there are hundreds of MM types. We wished to find some way to classify MMs to help understand cells as a whole. An evolutionary origin for cells would require this, since the starting point would have to be as simple as possible. Are some logic processors so indispensable they must have arisen earlier, and could others be added later?

We tried to develop a scheme based on necessary precedence, observing that some MMs require a preexisting foundation of other MMs. F_0F_1 ATP synthases can be built only if the necessary proteins are already available, suggesting ribosomes are more fundamental. However, we know that translation at ribosomes requires ATP to function, which implies the opposite precedence.

Additional examples we considered were also inconsistent with a hierarchical classification. Ribosomes function only once the whole complement of aminoacyl-tRNA synthetases (aaRS) are in place and mRNAs are being produced. However, both aaRS enzymes and RNA polymerases are constructed from proteins, so functioning ribosomes would need to already have existed.

This is significant since it implies an all-or-nothing design. This is inconsistent with an unguided evolutionary scenario, whereby simpler foundational MMs could somehow evolve first to prepare the ground upon which more complex MMs can arise. These foundational MMs, though, require the “higher-level” MMs. We must not overlook that foundational MMs such as aaRS offer no biological value alone. Attaching activated amino acids to tRNAs without a genetic code or ribosomes serves no purpose, and any organism wasting the raw materials and energy thus consumed would be at a selective disadvantage.

We propose tentatively a four-category classification of cellular information processors, where at least some members within each category can interactively

affect others within the same or the other categories (Figure 5).

i) Processors Used to Assemble Key Raw Materials

MMs in this category assemble components into more complex building blocks (e.g., proteins, DNA, RNA, lipid, and sugar polymers) and the MMs that manufacture high-energy molecules such as ATP, Pcr (Phosphocreatine), NADH, FADH₂ and NADPH. Examples include **ribosomes** (Staley and Woolford Jr., 2009); **DNA polymerases** (Garcia-Diaz and Bebenek, 2007; Federley and Romano, 2010; Hübscher et al., 2000; Wu et al., 2014); **DNA-dependent RNA polymerases** (Jonkers and Lis, 2015); **RNA-dependent RNA polymerases** (Ahlquist, 2002; Maida and Masutomi, 2011); **reverse transcriptases** (Ducrest et al., 2002); and **aminoacyl-tRNA synthetases (aaRS)** to charge tRNAs (Yadavalli and Ibba, 2012). We provide only some examples here and will not go into details but reiterate how many proteins are typically involved per MM. For instance, the aaRS core complex in multicellular eukaryotes is composed of 8 proteins with 9 enzyme activities and 3 auxiliary proteins (Norcum et al., 2005).

ii) Processors That Refine Raw Materials

Several molecular machines refine the location, concentration, half-lives, and other properties of biomolecules already assembled. Examples include **spliceosomes** (Nilsen, 2003); **hexameric AAA+ enzymes** (Hanson and Whiteheart, 2005; Bar-Nun and Glickman, 2012); **RNA helicases** (Jankowsky, 2011); **DNA helicases** (Sommers et al., 2015); **topoisomerases** (Nitiss, 2009); machines producing chromosome double-strand breaks followed by **homologous recombination** during meiosis (Baudat et al., 2013; Brick et al., 2012; Yamada et al., 2013); protein kinase c (**PKC**) (Steinberg, 2008); **proteosomes** (Bhat-tacharya et al., 2014); **apoptosomes/**

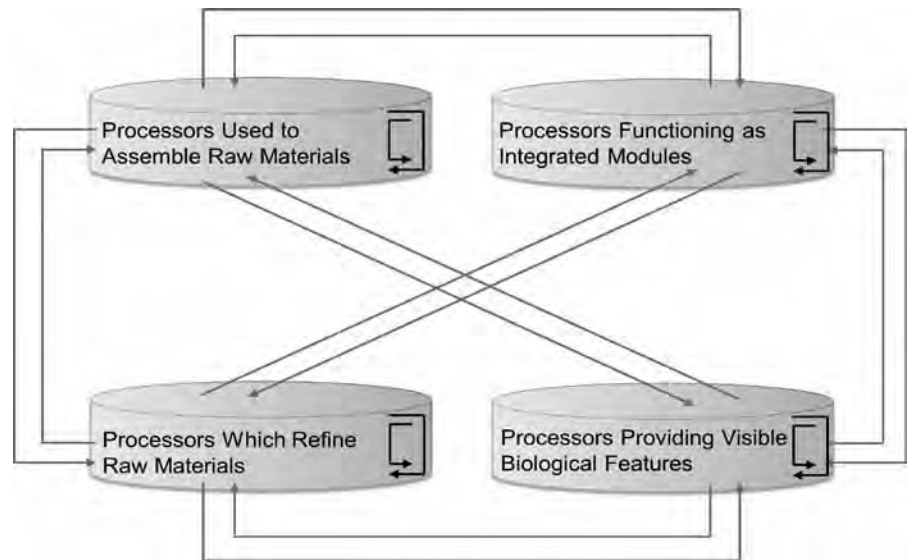


Figure 5. Model to classify cellular information processors. Members from each category can affect and be affected by the results of processors from the other three processors.

caspases (Rastogi and Sinha, 2009); **RNA degradasomes** (Bandyra et al., 2013) including RITS complexes (RNA Interference by Transcriptional Silencing) (Verdel et al., 2004; Verdel et al., 2009; Sugiyama et al., 2005); **kinesin motors** (Marx et al., 2009); **myosin motors** (Sweeny and Houdusse, 2010); **protein translocases** such as Tim/Tom Systems (Schmidt et al., 2010; Koehler et al., 1999); **ClpX** (a molecular machine that unfolds proteins and then transports them into another complex) (Baker and Sauer, 2012); the bacterial **SecYEG PreProtein** translocation channel (Lycklama and Driessen, 2012); **Hsp70** chaperone machines (Mayer and Bukau, 2005; Mayer, 2013); and **Hsp60** chaperone machines (Fink, 1999; Merendino et al., 2010).

iii) Processors Providing Services as Integrated Modules

Some MMs provide holistic cellular services that go beyond assembling and modifying biochemicals. Examples

include **calcium pumps** (Brini et al., 2013); **cytochrome C oxidase protein pumps** (Wikström, 2004; Yoshikawa et al., 2011; Yoshikawa and Shimada, 2015); **meiotic and mitotic cohesin complexes** to ensure accurate chromosome segregation during replication (Mehta et al., 2012; Maddox and Ladouceur, 2015); **condensin I and II complexes** (Hirano, 2012); **immunological synapses**, a complex cellular structure that forms at the interface of a T cell and a cell that expresses the peptide-MHC complexes (Dustin, 2014); **Smc5/Smc6 complexes** (Outwin et al., 2009; Farmer et al., 2011); **cytoplasmic dynein motors** (Allan, 2011); **MRX complexes**, which determine telomere integrity by a protein-counting mechanism (Lue, 2009; Ball et al., 2014); **F₀F₁ ATP synthases** (Long et al., 2015), which consists of at least 22 subunits (Nakamoto et al., 2008); bacteriorhodopsin (**bR**), the simplest known light-driven proton pump (Haupts et al., 1999); **hemoglobins** (Schechter, 2008); and **kinetochores**, for

```

public class TranslateCodons {
    public void ProcessEachCodon(String codon){
        String c = codon;
        switch (c) {
            case "GCU": {
                // 1: Delay translation by time reflected by this codon. E.g. try {Thread.sleep(10);} catch (Exception e) {}
                // 2: Transfer Alanine from the tRNA to the growing chain
                // 3: Release the attached tRNA from the codon
                // 4: Move the mRNA forward one codon position
            }
            case "CGU": {
                // 1: Delay translation by time reflected by this codon.
                // Java example try {Thread.sleep(35);} catch (Exception e) {}
                // 2: Transfer Arginine from the tRNA to the growing chain
                // 3: Release the attached tRNA from the codon
                // 4: Move the mRNA forward one codon position
            }
            //case n Code the rest of the cases
        }
    }
}

```

Figure 6. Some of the instructions being carried at the A site of ribosomes, identified by empirically observing what happens when each codon on mRNA is processed.

which over 80 protein components are involved (Cheeseman and Desai, 2008). These machines need not be physically connected into adjacent, cohesive units.

A matter to consider is whether there is a clear boundary between multicomponent MMs and integrated processes such as the Calvin-Benson cycle (11 enzymes; Michelet et al., 2013) and the TCA cycle (King, 2015).

iv) Processors Providing Visible Biological Features

Finally, it seems that some MMs comprise biological features whose value and operation are clear by simple observation even lacking understanding about the molecular mechanisms involved. Examples include **bacterial flagella** (Xie et al., 2011); **eukaryotic flagella** and

cilia, using over 360 different proteins in the case of green alga *Chlamydomonas reinhardtii*, (Pazour et al., 2005); **blood clotting** cascades (Adams and Bird, 2009); **antibodies** and the adaptive immune system (Iwasaki and Medzhitov, 2015; Schenten and Medzhitov, 2011; **apicomplexan glideosomes** (Boucher and Bosch, 2015; Fréchal et al., 2010); type I-VII chaperone–usher and the curli **secretion systems** (Costa et al., 2015; Douzi et al., 2012; Chatterjee et al., 2013).

Final Comments on Type I Cellular Hardware

The type I hardware discussed above is indispensable to process coded data in a cell that “either instructs or directly produces nontrivial function at its des-

tinuation” (Abel, 2011, p. 3). In Part I (Truman, 2016) we mentioned that in the genetic code, different codons can specify translation to the same amino acid, but these codons are not 100% interchangeable for all biological purposes. There are at least five “variables” known on ribosomes where logic processing occurs: at the **A** (aminoacyl), **P** (peptidyl), **E** (exit), **T** (elongation factor Tu), and **I** sites (initiation). At the **A** site the value of the variable is specified each time by a codon from an mRNA placed there, and then several logical operations are performed (Figure 6). One operation communicates which amino acid to add to the growing peptide chain.

RNA transcription elongation rates are also highly variable throughout different genes, which affect co-trans-

scriptional processes such as splicing, termination, and genome stability. This pausing, especially for Pol II, involves several transcription factors and complexes such as the NELF and DSIF in gene and sequence-specific ways (Jonkers and Lis, 2015). RNA interference is another example of an RNA code specifying processing steps. Binding of miRNA to excessive mRNA can prevent translation but may also recruit enzymes to actively degrade the mRNA (Francis, 2011, p. 130).

We now observe something remarkable from a computer design perspective. “Instructions” in cells such as how fast to translate each codon, to release the attached tRNA, and to move the mRNA forward one position, are not implemented using prescriptive, readable instructions in a source-code program but through precisely crafted biochemical features. These include the bonding strength between the tRNA’s anti-codon with the mRNA codon, the concentration of that particular tRNA present, and attachment of a high energy ATP at just the right time and place.

II. Hardware that Contribute without Codes

Two kinds of computer and cellular hardware are used to guide outcomes: those whose purpose is to process coded data (as discussed above) and those that operate primarily without codes, which we now consider.

In cells, far more hardware functions are integrated into the entire system than in computers. It is the nature of computers to provide value by running software programs that generate conclusions in symbolic form that humans or other programs to a major extent then act on. Individual self-replicating computers do not exist, needing to synthesize their own energy and their own internal hardware (cables, memory cards). Cells are to a much greater extent “their own customers” and need to physically act on

the symbolic conclusions made. It is not enough to calculate how much of which materials or energy need to be generated, or that repairs must be performed, or the timing of cell cycle phases. The cells must physically act on most of the consequences from these conclusions on their own.

Insights from CIS Theory

Human DNA consists of four possible nucleotides at around 3 billion base pair positions and bacteria of a few million base pairs. The coding capacity in terms of binary decisions is insufficient as the only source of guidance for organism development, continual decision making and internal cellular physical implementation, a concern that led to coded information theory (Truman, 2012a; Truman, 2012b; Truman, 2012c; Truman, 2013). Others are also concluding there are informational sources beyond what could be hard-coded on DNA.

Woodward and Gills (2012) wrote recently, “To be more specific, the zygote’s three-dimensional structure seems supremely important. Every molecule, every structure, every atomic nook and cranny of the zygote potentially contributes to the cell’s destiny” (p. 78). Francis (2011) also comments, “In the traditional view, genes function as executives that direct the course of our development. In the alternative view, which I advocate, the executive function resides at the cellular level and genes function more like cellular resources” (p. xiii).

DNA cannot directly specify all the things that occur such as the precise arrangement of all neurons, where and how which proteins interact, and the organization of the circulatory system, nor can it anticipate how to adjust our bodies for every step we might take.

Physical constraints designed into the CIS can decrease the contribution that needs to be communicated by coded messages by channeling possible outcomes. Here is an example: A coded message could instruct a robot which

decisions to take to transverse a maze. As a simplified example, we are to provide a coded message instructing whether to move Up, Left, or Right (Truman, 2015).

In Figure 7 the eleven-symbol message “UUULUULUULU” is used, where every position communicates a new value to a receiver decision variable. Assume that upon entering any of the cubicles in the last row a sensor at that location is activated, attaching a rope to the robot, which is then dragged to the destination. The minimum number of U, L and R symbols required to reach the most distant square (labelled X in Figure 7) would be twelve.

The sensor and guiding rope could be cleverly placed closer to the origin, requiring less informational contribution from a coded instruction (Figure 8).

In the extreme case, the intention could be satisfied using the rope only (Figure 9). The rope could mimic the turns expressed formerly by coded messages.

What might be overlooked in this example, but is fundamental to understand cells, is that there is considerable design and specification agreement up front, and the software effort can benefit from this foreknowledge: the environment the code must operate in is set, how to interpret each symbol is known, and physical factors prevent undesired behavior from occurring (e.g., gravity prevents the robot from moving upwards).

Let us elaborate. We know the size of the squares and that they are the same, so each length of advance can be identical when designing the equipment and the code. This implies the precise duration to continue in each of the three possible directions does not need to be communicated along with each symbol. Knowing the nature of the now constrained problem and equipment design, no search algorithms need to be included, whereas this might not be true of other possible designs. If we know movement can only be in two dimensions, exactly 90° or straight ahead, then corrective

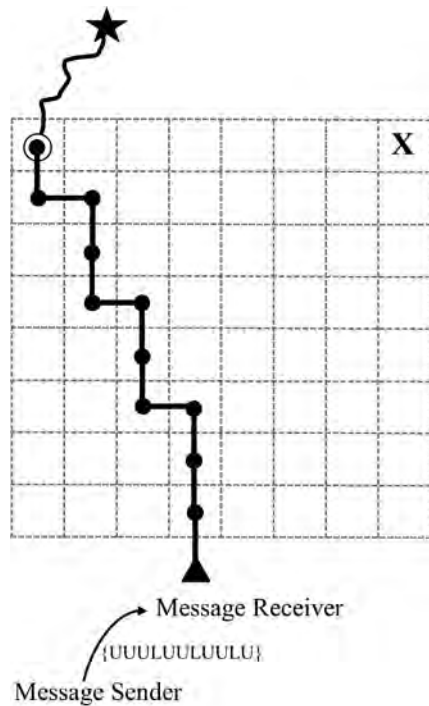


Figure 7. Coded messages consisting of U, L and R (Up, Left, Right) can instruct how to traverse a maze. At least twelve symbols would be needed to reach the most distant point labelled X.

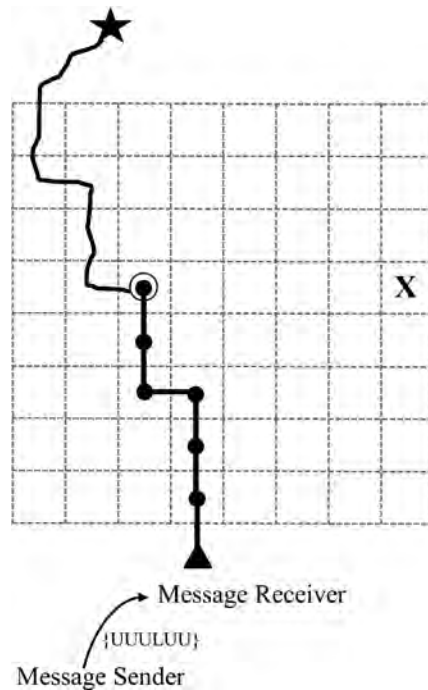


Figure 8. If the guiding rope is placed optimally in the fifth row, nine combinations of U, L, R suffice to reach the most distant point (marked X), from which correct exiting would be ensured with the help of an attached rope.

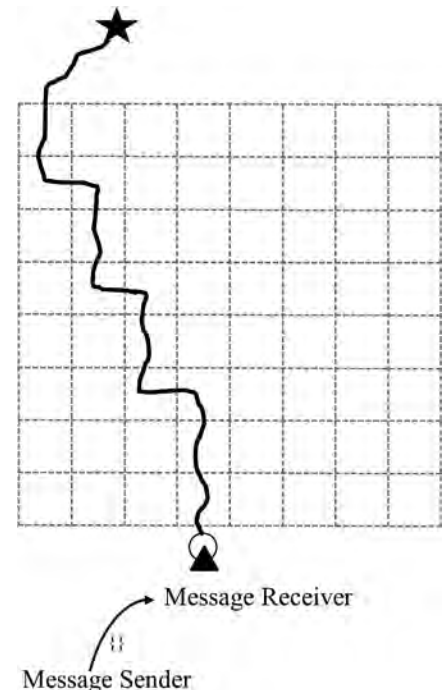


Figure 9. If the guiding rope is placed right at the entry point of the maze, no additional coded message would be necessary to traverse the maze.

instructions will not be needed. All these contributions permit sending the robot to any destination using very simple coded messages.

There are many biological analogies, such as when some mRNAs “automatically” delay translation or are stored and often transported to where translation should occur (Anderson and Kedersha, 2006). Another example involves ribosomes being created near where the mRNAs should be translated or are transported by kinesins along microtubule pathways. Other examples include the separation of chromosomes by spindles into precise locations for physical mechanical reasons before ending up in daughter cells during mitosis, and signal transmission along neurons. Movement in the maze ex-

ample was constrained to a few adjacent squares in only two dimensions, but specifying in three-dimensional detail reliably where everything should be sent in a cell and when using only coded messages would be a nightmarish requirement.

Emergent properties do arise that need not be implicit in physical properties of individual components used by a system (Lehn, 2002). Turning the ignition key of a car initiates a series of processes that include combustion in a useful manner, resulting in “emergent properties.” The same is true of biological systems, in which judicious preparation of the necessary components automatically results in the intended outcome without additional active coded informational guidance.

Although a multitude of coded parameters are used by cells to specify intention, they operate in the context of many designed physical constraints that significantly prevent erroneous behavior. Even diffusion of second messengers such as calcium, nitric oxide, carbon monoxide, lipophilic molecules (diacylglycerol, ceramide), superoxide, hydrogen peroxide, and hydrogen sulfide—presumably a Brownian type random movement—has been optimized in many ways. They are small and of appropriate solubility in a fluid environment to facilitate motion and will only need to explore restricted volumes using multiple copies and a high concentration of potential targets.

Cells possess several components that contribute toward correct (and

prevent incorrect) behavior. In the few examples mentioned next, we will see a recurring theme: the informative contribution of the assemblages is far greater than was provided by the coded messages used to put them together and to interact with them. There is a leverage effect. For example, a certain kind of membrane can usefully constrain a vast multitude of the appropriate kinds of bio-substances to a relevant region.

Cytoskeleton

The cytoskeleton is composed of proteins that can form long fibers and interact with cell membranes (Doherty and McMahon, 2008; <https://en.wikipedia.org/wiki/Cytoskeleton>). The designs in eukaryotic cells are particularly elaborate, where different proteins are used to form the microfilaments, microtubule, and intermediate filaments. About 70 proteins are used to build intermediate filaments, and all except crescentin are found only in animal cells (Herrmann et al., 2007). The cytoskeleton can interact with hundreds of other proteins, such as cross-linkers, capping proteins, nucleation promoting factors, and signaling molecules (Huber et al., 2013; Fletcher and Mullins, 2010).

The cytoskeleton provides indispensable services. Entire chromosomes are moved to daughter cells during replication (i.e., millions of individual nucleotides benefit as an ensemble), cell and organelle shape and volume are maintained, intracellular transport of entire organelles and vesicles are performed (i.e., with their entire biochemical content), the location of some macromolecules is constrained, portions of the cell are connected along which myosin-based motors can be guided, and the nuclear lamina is strengthened.

A few special signals guide the creation of these kinds of constraints. For example, microtubules grow in many directions until they encounter a signal on a membrane wall, at which

point stabilizing agents lock the end of the microtubule in place (Kirschner and Gerhart, 2005, p. 151). As another example, vascular endothelial growth factors determine where new blood vessels are to develop, ensuring cells in most need of oxygen are supplied best (Kirschner and Gerhart, 2005, p. 169).

Pathways in retina to guide photons

In addition to the cytoskeleton discussed above, there are other examples of processes being guided by constraining physical pathways, such as the circulatory system, neural pathways of somatosensory perception, and brain neural networks. Photon signals that land on any of the estimated 260 million photoreceptors are transferred via 2 million ganglion cells on to the central nervous system (Gazzaniga et al., 2009, p. 178). Once the pathways are in place—during the organism's development and later learning—many of the activities that occur every second are largely automatic, and subsequent logic processing of the signals being received is thereby simplified. If photons were to land all over the place and not be guided to where interpretation is to occur in the brain, it would be close to impossible to make sense of these signals.

Organelles

As an example organelle, we will mention peroxisomes, which degrade fatty acids and eliminate toxic hydrogen peroxide in the cell. To do this, numerous enzymes are imported from the cytoplasm and concentrated together to work effectively (Montilla-Martinez et al., 2015). Here again we see the collaboration of CIS factors, since codes are also involved (Truman, 2016, Figure 1). Proteins to be transferred to peroxisomes carry certain signal sequences, called PTS1 and PTS2, which are recognized by import receptors. All the necessary participants are then forced conveniently close together within the organelle space.

Protein containing subcompartments

Ribonucleoproteins form discrete cytoplasmic RNA granules in germ cells (“polar” and “germinal granules”), somatic cells (“stress granules” and “processing or P bodies”) and neurons (“neuronal granules”). These are involved in many processes, including mRNA localization and degradation, posttranscriptional modulation, and epigenetic gene expression (Anderson and Kedersha, 2009; Anderson and Kedersha, 2006; Kiebler and Bassell, 2006).

The eukaryotic nucleus contains subnuclear compartments such as the nucleolus, interchromatin granules (ICGs), PcG bodies, cajal bodies, perinucleolar compartment, and PML bodies, where special processes are coordinated (Spector, 2001; Shapiro 2011, p. 38; Osborne et al., 2004). Many steps in the DNA-damage repair process demand a careful spatial and temporal synchronization of events (Misteli and Soutoglou, 2009) carried out in “repair centers” (Lisby and Rothstein, 2005). The structures in the eukaryote nucleus, where specific and repetitive processing such as replication, transcription, and repair occurs, are referred to as “factories” (Mitchell and Fraser, 2008; Razin et al., 2011).

As with virtually all cell process, additional guidance within the subcompartments is provided by coded messages usually in the form of sequence patterns. There are signals called S/MARs (surface/matrix attachment regions) that communicate the sites for localization to the nuclear lamina (Meuleman et al., 2013). However, it is also true that location and concentration of the correct components are ensured through purely physical principles once the engineered parts are assembled into a functional unit.

Lipid rafts

These are heterogeneous domains with high levels of cholesterol and sphingolipids on membranes that result in

different protein composition. The rafts are defined as “small (10–200 nm), heterogeneous, highly dynamic, sterol- and sphingolipid-enriched domains that compartmentalize cellular processes. Small rafts can sometimes be stabilized to form larger platforms through protein-protein and protein-lipid interactions” (Pike, 2009).

Lipid rafts are more ordered and tightly packed than the surrounding bilayer and seem to float in the membrane bilayer. Although more common in plasma membrane, lipid rafts have also been identified in lysosomes and the Golgi apparatus.

This special environment within membranes can facilitate various processes in eukaryotes, such as cell signaling (by increasing the chances of the necessary protein-protein interactions), protein trafficking, and regulation of neurotransmission (Simons and Ehehalt, 2002).

Membranes and pores

Larger molecules such as amino acids, glucose, and nucleotides have a difficult time passing through membranes, so their location can be controlled by these barriers, alleviating the need for coded messages to specify this restriction in location. The surfaces of membranes can also be used for other purposes, such as helping to silence inactive chromatin (Walhout et al., 2013, p. 138) (Figure 10).

Eukaryotes have about 2000 nuclear pores—each composed of over 30 machinelike parts (Woodward and Gills, 2012, p. 40)—that permit transport of various substances in and out. In addition, ion channels permit the movement of ions like Na^+ , K^+ and Ca^{2+} across membranes at a controlled rate, for example, by using a limited number and location of these channels.

Concentration gradients

Concentration gradients can act as informational signals. In the nervous system,

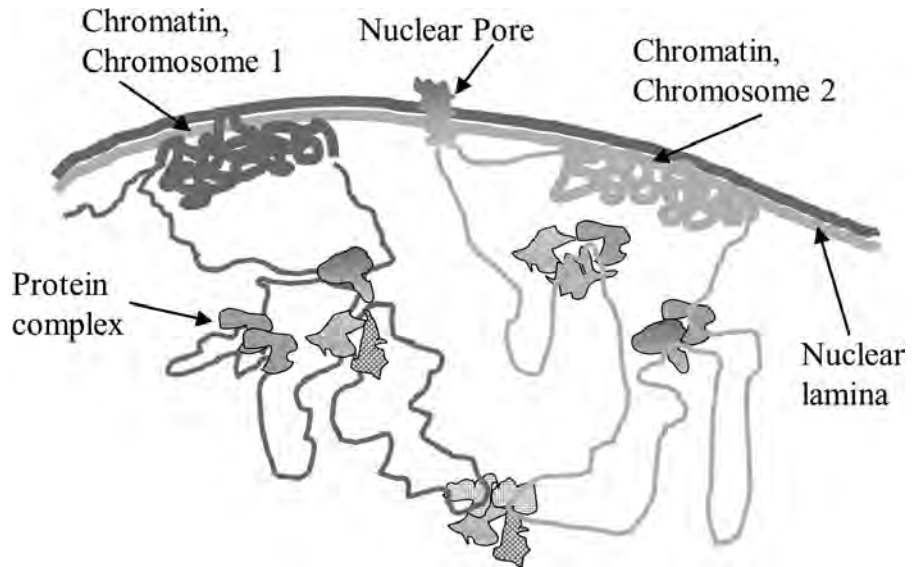


Figure 10. The surface of the nuclear lamina can help deactivate transcriptionally inactive chromatin (shown in heavier lines for two different chromosomes). Regulatory and active genes from the same or different chromosomes can be concentrated together in the nuclear interior using protein complexes.

nerve cells develop in many directions but soon undergo suicide (apoptosis) unless they enter a region possessing enough of a “survival factor” such as growth factors and cytokines (Fuchs and Steller, 2011; Portt et al., 2011).

Morphogens such as activin, bone morphogenetic protein (Bmp) 4, sonic hedgehog (Shh), and bicoid (Bcd) act as graded positional cues that control cell specification in developing tissues. Most are protein ligands that bind to transmembrane receptors and initiate intracellular signal transduction cascades to regulate the transcription of specific target genes (Ashe and Briscoe, 2006). To be a morphogen a concentration gradient of the substance must be able to generate at least two distinct cell types. These ligands can establish the initial polarities of embryos and specify cell identity in tissues by communicating their position with respect to the source of the signal.

Other concentration gradients produce their effects through more obvious physical-chemical reasons. Water moves

automatically toward hypertonic regions (regions with high concentration of dissolved substances), and ions like Na^+ , K^+ and Ca^{2+} naturally flow down their concentration gradients. (The Na^+/K^+ ion pump moves Na^+ out of the cell and K^+ in, against their concentration gradient, using energy provided by ATP.) Some passive transport is also facilitated by transport proteins in the membrane, but much guidance seems to be provided by the concentration gradient, a strictly physical factor that still needs to be properly organized.

Chemical binding

The need for coded instructions is decreased dramatically by ensuring that only a subset of possible chemical reactions can occur. Only the 3'5' phosphodiester bonds are permitted in nucleic acids to form the DNA and RNA backbone and only peptide bonds in the case of protein chains. Since the other reactions have deliberately been excluded from the cell design, the particular kind of reaction to perform

does not need to be specified by coded instructions.

Binding strengths

It is easy to overlook that cellular codes benefit by being able to make assumptions (recall the discussion above on the labyrinth). If the decoding procedures should be unreliable for any of the codes, the coded instructions would need to be far more complex, having to check current states and take corrective action. Current states are indeed checked by cells for complex processes, for example in the cell cycle. To illustrate, suppose the genetic code was highly unreliable for any of many possible reasons, one example being that ribosomes had not been precisely engineered to operate on nucleotides as triplets, leading to translation frameshifts. The system design would now need all kinds of error-correcting logic.

The cellular design, however, has already taken this critically important factor into account, by using binding interactions and dimensions that are just right for all the codes. Consider how epigenetic tags must be added and removed reliably, in some cases easily (histone code: see <http://www.cellsignal.com/contents/resources-reference-tables/histone-modification-table/science-tables-histone>) while in other cases with much more difficulty (e.g., methylation of DNA). The codon-anticodon strength plus supportive context in ribosomes ensures an interaction strong enough to ensure reliable identification but not so strong the mRNA would often stall. There are many examples of this “just right” principle that the codes implicitly rely on, such as the TF to CRE interactions, DNA-DNA base pairing strength, histone to DNA interaction, phosphorylation to proteins, and so on.

Location of synapses

Guidance of action potentials along neurons are dramatically aided by having the presynaptic terminals (where neu-

rotransmitter molecules are released) already located at the ends of axons, strategically very near the postsynaptic neuron.

Correct range of pH, temperature, viscosity

Cells regulate their internal environment in many ways, including pH, temperature, free radical content, waste products, and viscosity. This automatically lowers the entropy with respect to a reference state lacking these controlling factors, thus circumventing the need for coded instructions to avoid the unwanted possibilities.

Cells interacting as ensembles

Striated or skeletal muscles consist of several cells that have fused together. They are excitable by neuronal stimulation, which causes them to contract, but the direction and range of possible behavior have already been established using physical constraints. For example, they do not need special instructions for how to restore the resting length since they have suitable elastic properties (Frontera and Ochala, 2014).

Discussion and Conclusions

In Part 1 (Truman, 2016) we saw that cellular processes are controlled using Boolean logic and many codes, each with their own data types, data structures, and operations. The resemblance to software used by digital computer is inescapable. Here in Part 2 we complete the picture by discussing the hardware aspects of the cellular information processing systems, necessary to instantiate the symbolic formalism and to provide physical constraints to ensure the correct outcomes.

The cell must be understood as a holistic entity. We agree with Moss's view: “I have begun to marshal evidence on behalf of the idea that cellular context as a whole is basic to the nature and continuity of living beings and is irre-

ducible to any of its constituent parts” (Moss, 2004, p. 95). The guidance is not provided by a blueprint or detailed prescriptive language on DNA, a notion associated with the theory of preformationism prevalent in the eighteenth and nineteenth centuries (Francis, 2011, pp. 120, 126; Oyama, 2002, ch. 3). An example by Francis (2011, p. 86, 111) demonstrates this. Most (tens of millions) of epigenetic methyl tags are removed during the process of making animal eggs and sperm. Then the methylation patterns are restored in the egg and sperm cells before fertilization. Obviously, the guidance to restore the pattern must have come from an informational source other than the now methyl-free DNA. Then after fertilization, but before implantation, many of the methyl tags are removed again. In the case of plants, epigenetic tags developed during a lifetime can be stable over hundreds of generations, since epigenetic reprogramming is much less pervasive (Francis, 2011, pp. 87, 90).

Challenge to Produce One New Protein by Chance

A large variety of proteins from unrelated protein families are needed to build molecular machines (and often long RNA chains are also needed). The vast majority of random polypeptide sequences, however, are unsuitable for biological purposes, but until a new protein provides a measurable level of functionality, natural selection cannot favor that organism. One way to estimate the proportion of useful to worthless sequences is to recognize that globular proteins must first be able to fold reliably so that the various steric and electronic features are located reliably every time that protein is produced.

Douglas Axe replaced small clusters of side-chains randomly starting with a weakly functional β -lactamase domain to estimate the proportion that fold. Taking into account that about 10^4 protein fold types exist in cells, he concluded

that roughly 1 in 10^{74} domain-sized sequences fold reliably (Axe, 2004, 2010).

The literature on folding proportion was reviewed in a series of six papers in the *Journal of Creation* (Truman, 2012a) that concluded that the only unambiguous cases of folded artificial proteins produced in a lab so far had been intelligently designed. This guidance came from scientists applying a deep understanding of optimal polypeptide sizes to permit folding (considerably smaller than a median sized protein) and which amino acid patterns favor formation of necessary substructures for folding, such as α -coils and β -sheets.

The literature needs to be interpreted carefully. Polypeptide chains can form semi-structured but still basically amorphous molten globule states with various collapsed conformations, crude cooperative unfolding, and secondary structures. It is not surprising that various polypeptide sequences reveal through spectroscopy some secondary structure in some randomizing experiments, but a few random α -helices and β -sheets produced, of different sizes and locations each time a polypeptide sample clumps together, is not the same thing as a protein reliably and identically folding to a single state.

Three general approaches have been used to estimate this proportion (Truman, 2006): (1) designed “semi-random” chains of amino acids are generated to see if any show evidence of folding; (2) existing protein sequences are mutated to see how much change is tolerated; (3) sequence variability across organisms is compared. The available estimates range widely, with the examples discussed ranging between one out of 10^{44} to 10^{112} (Truman, 2006).

As an example experiment conducted at MIT, one to three codons were varied at 25 positions along a 92-residue portion of a 237 amino acid γ -repressor (Reidhaar-Olson and Sauer, 1990). For only the 92-residue portion examined, a proportion of about one

out of 10^{63} sequences was estimated to be functional. In a recent study using 71 residue random-sequence proteins with overall composition tailored to resemble globular proteins, the authors commented that “a mere 5–20% of a given protein’s amino acid sequence remains invariant during evolution,” implying that forming proteins by chance is easy (LaBean et al., 2011).

But let us examine LaBean’s estimate. Assume 5 to 20% must be invariant and every other combination in 80–95% of a protein could be acceptable. Then each kind of protein with median length 250 residues would only need to have $n = 12.5$ to 50 residues placed correctly, where each position would have a chance of about $1/20$ being correct by chance (depending on the model assumptions, such as prebiotic amino acid proportions, or a genetic code). $(1/20)^n$ for $n = 12.5$ to 50 implies a proportion of only 10^{-17} to 10^{-65} . The reality, however, is that only a small proportion of proteins having the remaining 80 to 95% positions totally random would still fold reliably, so the proportion on average is surely many orders of magnitude smaller than 10^{-17} . Even small proteins such as cytochromes (only 104 residues) show identity at 26 positions for all the sequences available (Bray, 2009, p. 141), and $(1/20)^{26} = 1.5 \times 10^{-34}$.

To put the analysis in perspective, using optimistic evolutionary assumptions demonstrates that the maximum number of polypeptide candidates that could have been generated by living organisms would be about 10^{46} , spread throughout all organisms and over more than four billion years (Truman and Heisig, 2001). To produce a single new, minimally functional molecular machine, many unrelated proteins must be present at the same time, proportion, and location only to satisfy the hardware portion of the processing requirements.

Using the highest proportion of 10^{-17} from above would imply odds of obtaining a single copy of three different folded

proteins as $(10^{-17})^3$ or (10^{-51}) , and these must be all located together at the same time and place and somehow jointly happen to do something biologically useful. Recall that at most 10^{46} organisms ever lived. How could ribosomes, RNA and DNA polymerizes have been produced by chance?

A new complex machine such as a spliceosome would also require that the corresponding software components be in place: separating introns and exons requires the correct signals at the right place and that false positives not be spread all over the genome.

When analyzing molecular machines one should consider the size of the proteins used to create them, since larger proteins are much more difficult to form by chance. As an orientation, the median number of amino acids composing proteins has been calculated to be 361 for Eukarya, 267 for Bacteria, and 247 for Archea (Brocchieri and Karlin, 2005).

Decoders Must Be Inheritable

During mitosis, copies of the various coded data plus functioning copies of the decoding MMs all need to be replicated correctly for the daughter lineage to still function and preserve the cell type. It staggers credibility to argue this could have arisen through random mutations. For example, to replicate a pattern of 100–200 million methyl groups, specialized protein methyltransferase enzymes must already exist and be assembled at the site during creation of the new DNA (Woodward and Gills, 2012, pp. 113–114). As a second example, while a new copy of DNA is being synthesized, millions of the 8-histone spools are also manufactured for the new DNA (Woodward and Gills, 2012, p. 60).

Repair Mechanisms

Reflection shows neo-Darwinian theory (NDT) is inadequate to explain the origin of sophisticated computational machines like cells, with elaborate logic

processing, multiple codes and many very complex collaborating decoders. They are functioning von Neumann self-replicating automatons (Barbieri, 2003, p. 25). This kind of complexity is foreign to inanimate matter and until carefully set up to be adaptable and self-correcting would quickly collapse as a viable system. More than 10,000 DNA damage events occur daily in every cell in the human body, and if left to itself, a malfunctioning (cancerous) cell would spread the damage. We survive because our cells possess about 10 different DNA repair pathways, designed to handle particular lesions (Mullins et al., 2015).

Error correcting processes—such as double-strand break (DSB) (Brissett and Doherty, 2009) and nucleotide excision repair (NER) (Harfe and Jinks-Robertson, 2000)—probe the genome for endogenous and exogenous damage, and must be able to recognize special patterns that signal damage, which incidentally represent yet another code. Codes and processing equipment are ubiquitous in cellular repair. Noncoding RNAs are expressed in response to damage (Chowdhury et al., 2013) and a number of phosphorylation, acetylation, methylation, ubiquitylation and chromatin-remodeling codes are used to demarcate the lesion site. These provide the informational input to first assemble and then break down the required repair machines (Gospodinov and Herceg, 2013; Hitomi et al., 2007; Marteiijn et al., 2014; Panier and Durocher, 2013). Damaged DNA is often mobilized to subnuclear repair centers (Shapiro, 2011 p. 46; Bekker-Jensen and Mailand, 2010; Lisby and Rothstein, 2004), another example of the dynamic interaction between informational parameters and dynamic hardware processors.

Genome Truncation

A final reason we'll mention for the irrelevance of NDT involves the requirement to start simple and increase complexity. Many complex molecular

machines, such as spliceosomes, are only found in eukaryotes, which supposedly arose long after prokaryotes, so the theory must explain the origin of dramatic innovations and much larger genomes. Eukaryotes have far longer generation times and much lower population sizes, so considerably fewer than 10^{46} complex organisms would have been available to produce a multitude of novel proteins *de novo*. Needed are not trivially different protein sequences but proteins distributed among very different protein families. At least 4909 protein families are used in biology (Punta et al., 2012).

NDT is all about competitive replication from common ancestors. This poses a big problem. For small prokaryote organisms having around 1000 genes in the distant past, individuals expressing unnecessary genes would be disadvantaged, and streamlined competing individuals or species would soon out-populate them. The components of new molecular machines (without which the new codes would be worthless) would have to offer a net and immediate benefit above the disadvantages of longer chromosome replication times and greater energy plus material demands.

The new systems could not develop step-wise, waiting millions of generations for future fortuitous mutations to eventually generate a minimal level of selectively measurable functionality. The only way to compete against sister species in that immediate environment would be to truncate genomes, by eliminating whatever genetic material is not needed at the moment. Bacteria constantly eliminate DNA, and genome streamlining is a well-known phenomenon (Wagner, 2005, 2007; Truman and Terborg, 2008a, 2008b).

Neo-Darwinism Fails to Explain the Origin of Logic Processing

Neo-Darwinian theory remains the dominant naturalist evolutionary theory

and assumes all extant life evolved from a common ancestor, despite ever-increasing gaps in credibility. Historically it developed from a philosophical desire to deny the activity of a creator. Shapiro, from the University of Chicago, pointed out that “this insistence on randomness and accident is not surprising. It springs from a determination in the 19th and 20th Centuries by biologists to reject the role of a supernatural agent in religious accounts of how diverse living organisms originated” (Shapiro, 2011, p. 1).

Müller, from the University of Vienna, summarizes well where the theory now stands:

In the neo-Darwinian world, the motive factor for morphological change is natural selection, which can account for the modification and loss of parts. But selection has no innovative capacity: it eliminates or maintains what exists.... The inability of evolutionary theory to account for phenotypic organization has been recognized by numerous authors, with regards to both biochemical and morphological evolution. (Müller, 2003, p. 51)

In general, whenever we come across the terms “convergent evolution,” “genetic piracy,” or “exaptation,” we will discover a failure of neo-Darwinian theory and in most cases novel logic-processing elements which produce the same kind of biological feature. Müller goes into a detailed and very illuminating analysis of how “homology of a character in different species does not mean this character is generated by identical developmental processes, is controlled by the same genes” (Müller, 2003, p. 56) and admits to “the growing tendency to reject homology as a serious scientific topic” (p. 56). In the same book, Britten concludes that the prospects of finding a tree of life has become ever more remote, as more genomic sequences of microorganism have become available (Britten, 2003, p. 79). Of what value is a theory that fails to provide research

guidance or consistent interpretative methods?

In discussing the case of the octopus and the human camera eye, Kirschner and Gerhart (2005, p. 240) point out that the eyes derive from different tissues by different developmental means and are based on completely different phototransduction circuitries. Müller makes the same point (Müller, 2003, p. 57). Nevertheless, both use eye designs having the same pigment (rhodopsin) for photoreception, and both send electrical signals to the brain. Most now agree that a common ancestry for this kind of eye makes no sense, especially since organisms similar to the octopus do not share this feature, so the word “convergence” is used, which actually explains nothing whatsoever.

Remarkably, Kirschner and Gerhart (2005, pp. 253–254) claim tubulin and actin proteins must have been present in a common ancestor of prokaryotes and eukaryotic cells on the basis of having virtually the same three-dimensional structures even though they have almost zero sequence resemblance. The evolutionary interpretive methodology apparently permits picking and discarding what is due to common ancestry versus convergence on the basis of whichever seems to cause the least difficulties.

Having recognized that assuming common ancestry has provided him with no guidance, Müller continues asking the right questions and comes up with a sensible conclusion. “I propose that homology is not merely a concept or a conceptual tool, as it is often understood, but rather the manifestation of morphological organization processes. It thus represents a major, unresolved problem in evolutionary biology” (Müller 2003, p. 51).

The words “evolution” and “natural selection” have been given unbounded creative powers. Müller is now assigning a similar role to the word “homology.” It is a placeholder for an organizing principle that has been instantiated in many

ways but with a purposeful outcome which humans are able to recognize. “Homology is the manifestation of an ordering principle in morphological evolution ... This legitimate and strangely neglected scientific question lies at the center of the phenomenon of organismal evolution: it is not satisfactorily answered by current evolutionary theories” (Müller, 2003, p. 58).

What could these organizational processes be but a judicious application and reapplication of the kinds of common software and hardware informational principles we have been discussing?

NDT offers no solution to the existence of logic processing found throughout cells or the putative dramatic increase in complexity over time. In fact, it must assume a miracle again and again to permit conceptual starting points. Systematic genomic comparison studies are leading to the view (Lerat et al., 2004; Lerat et al., 2005) that a core of about 100 different genes are indispensable in all organisms. Anything less than this would not work. These core genes plus a few hundred others that may be somewhat exchangeable would have to be regulated and operational in a membrane protected up-and-running system. A few hundred genes’ worth of DNA on their own in a fluid environment will perform no biochemistry; they will simply be a dead polymer like a wet piece of plastic. This poses an insurmountable barrier for natural processes to produce a minimal organism able to survive and reproduce reliably.

Excluding a determined philosophically prior commitment, there is no solid scientific basis to believe unguided natural processes could or have created what hundreds of thousands of scientists cannot. As Bray pointed out, “Not only are biologists incapable at present of manufacturing the enzymes, membranes, and organelles needed for these processes; they still do not fully understand how they work or are put together” (Bray, 2009, p. 207).

We agree with Abel that “formalism not only describes, but preceded, prescribed, organized and continues to govern and predict Physicality” (Abel, 2011, p. 325). Cells, like all information-processing equipment, require a cognizant designer.

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The Apparent Age of the Time-Dilated Universe II: Gyrochronology, Magnetic Orbital Decay of Close Solar-Type Binaries and Errata

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Abstract

In creation time-dilation cosmologies, one major question is this: What maximum apparent age should be used to characterize the universe? In this paper, one particular age indicator is used. My larger plan is to determine estimates of the answer to this question for many age-bearing processes and then to give a reasonable answer to this question. In this case, I am pursuing astrochronology, the precise derivation of stellar ages from the orbital periods of single stars and interacting binaries. Here, I correct the earlier study (Samec and Figg, 2012) and expand the results using a simpler algorithm that applies to many more binaries. I increase the number of binaries in the earlier study from 18 to 124. The only basis for the selection of these systems is that they appear to be undergoing a clear and preferably long, decaying orbit indicative of magnetic braking. This is shown by a negative quadratic term in dP/dt (days/year), where P (days) is the orbital period of the binary. As before, I attempt an age estimate of these solar-type binaries apart from evolutionary time constraints assuming an initial period at the creation (or formation) of the binary (here, 5–20 days). This time a simpler kinematic approach is taken to extend the number of systems surveyed.

Introduction

Tian et al. (2009) noted that the rate of decay of orbits is 1–2 orders of magnitude faster than expected in binary star evolution (e.g., Guinan, Bradstreet, and Robinson, 1987). Although I find that this is nearer to 2–3 orders, their general observation is correct; that is, binaries are evolving at a rapid and easily

observable rate. This paper is a follow-up to our pilot study for this project (Samec and Figg, 2012),

Thus, binary evolution occurs in real time—easily perceptible by human observers. Although I correct a calculation error that occurred repeatedly in Part I, this basic result remains true.

In review, *astrochronologies* are those dating methods used to determine the age of an astronomical object. In evolutionary astronomy, these schemes are usually biased by the assumption that the age of the Sun is 4.57×10^9 years or 4.57

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Gyr. I call this the solar-age condition (SAC). The SAC is derived from the maximum radioisochron age of “primordial” meteorites. The term used to describe this particular study is *gyrochronology*, which is a derivation of stellar ages from the orbital period of solar-type stars and interacting binaries. The important result of the RATE (Radiosotopes and the Age of The Earth) project (Vardiman et al., 2005) was that isochronal dating is faulty, and actual geological ages are nearer to the chronology given to us in the early chapters of Genesis. The discrepancy—thousands of years versus billions of years—is due to an accelerated radioisotope decay rate occurring early in earth’s history. Standard geology assumes that the present decay rate is the same as it was in the past (“the present is the key to the past,” or uniformitarianism). This important study, yielded the age of the Earth and its surrounding solar system nearer to 7000 years than ~4.6 billion years.

Whereas the RATE results pertained to geological time-scales, I am finding a different time effect in astronomical time-scales. The cause is not *accelerated aging* but rather a difference in earth-bound clocks as compared to cosmological ones. In *Starlight and Time* (Humphreys, 1994), general relativity was used for the first time to solve the light-travel time problem: how can astronomical observations be made of objects billions of light-years away in a young universe? Humphreys’ answer to this dilemma is that time dilation occurred in the earth-based observational frame.¹ In his first model, earth-based clocks ran slowly when a collapsing white hole² (or black hole in his newer cosmology) event horizon passed the earth. During these moments, light not only came from the deepest realms of space to earth, but the aging of physical processes passed as the light traversed the distances through the universe to the earth-based observer. That is, a million light-years of light travel resulted in a million years of aging. In subsequent work, Humphreys found that when the earth was in the interior of a white or black hole, it was in a timeless region (Vardiman, and

Humphreys, 2011). So long as the Earth was inside the event horizon, objects outside of it continued to age and their light continued to impinge upon the earth. A mature cosmos was left in its wake. This was followed by the complete evaporation of the white hole and the termination of the event. During the event, in the frame of reference at cosmological distances, great ages passed, while in the earth time frame only a few days or less of time was experienced. This event may well have happened inside of Creation Week. An attempt is made here to determine the apparent age experienced by the universe outside the Earth’s time frame or, “What apparent age can I use to characterize the universe?” The 13.80 billion-year answer provided by the big bang community (Ade et al., 2015) should not be accepted due to its false assumptions, which are at odds with biblical history of the Earth. The biblical basis for a recent creation has been covered elsewhere (see Morris, 1993, pp. 19–20). But the acceptance of general relativity, which is proven as well as any of today’s scientific theories, with its time-dilation physics is certainly allowed, especially with the detection of merging stellar black holes with LIGO using GR predicted gravitational waves (Abbott et al. 2016). Clearly, the acceptance of man’s invention of the inflationary universe (Guth, 1997) or the cold dark matter model (Ade et al., 2015) is certainly not a part of my quest.

In addition, I will seek to avoid the use of the SAC in our observational studies. I prefer to base our timescales on natural reference clocks (NRCs) rather than clocks calibrated with the SAC. Such chronometers include Newtonian orbital periods, the speed of light, and situations where the physical rates, frequencies, velocities, and accelerations are known from observations (see Samec, 2011). In the Samec study, an apparent age in the range of 10^6 – 10^8 years was determined. In a similar study, spiral windup times as indicated by Humphreys (2005) gives an apparent age of less than **a few hundred million years**. This apparent age is only ~2% of the accepted evolutionary age of the universe.

¹ I am using Russ Humphreys’ first cosmology as an example of a creation cosmology, not as the defining one. I understand this model, so it is particularly easy to use. And I think that it has been around so long that it is most understood by the readers. I do not mean to not “prefer” it above the rest.

² Regarding White Holes: “Recent research discussed by Polchinski (2015) indicates that cosmologies based on event horizons, as with White Hole Cosmology, may need revision. However, the results of this line of research may not be known for some time, hence we continue to use these cosmologies based on classic general relativity, not on unknown improved theory needed for strong gravitational fields on the basis of quantum effects.”—The editor.

Magnetic Braking

As in Part I (Samec and Figg, 2012), I use the orbital decaying process of magnetic braking to determine ages. This is described fully in Part I. Binary stars consist of two stars that orbit about a common center of gravity (barycenter) and have a common orbital period (tidally locked, circular orbits). With time, the entire binary steadily loses angular momentum via magnetic braking. As this happens, the orbit shrinks and by Kepler’s third law, the orbital period shortens (see Figure 1). When the atmospheres of the stars touch, the stars are called *contact binaries*. The stars continue to coalesce into fast-rotating single stars such as A-type stars or subgiants, like the spotted FK Coma stars.

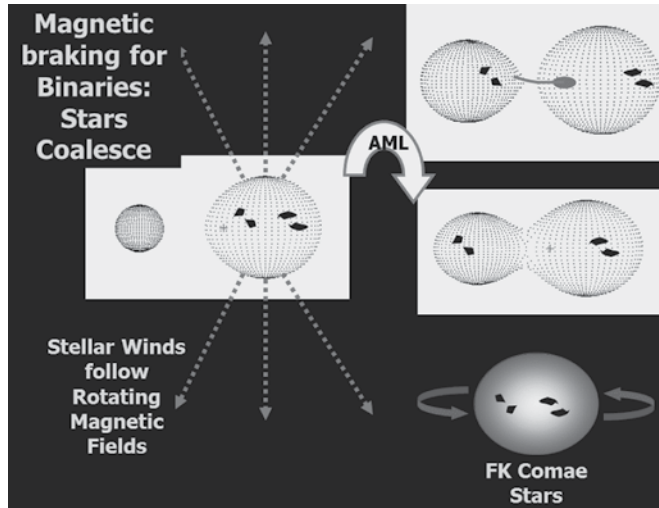


Figure 1. Magnetic braking on single stars. AML is an acronym for Angular Momentum Loss or “spin.” As the binary undergoes AML, the orbital period will decrease due to Kepler’s law.

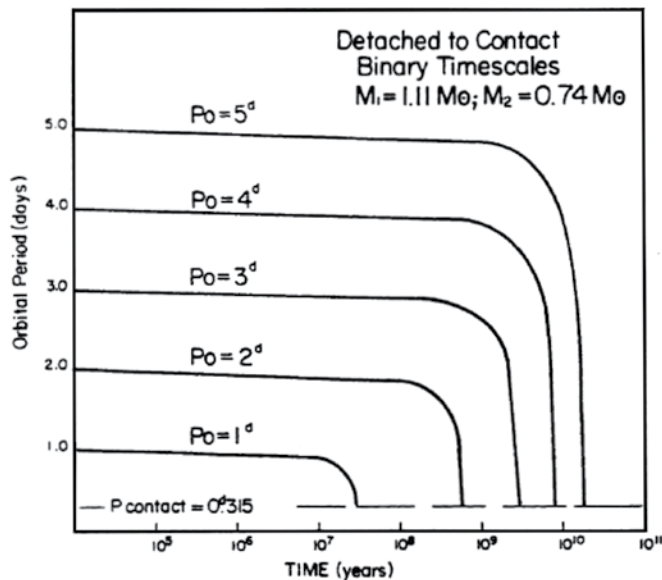


Figure 2. The time needed to brake from a, 1–5 d period binary to a 0.315 period binary with masses of 1.00 to 5.00 (Guinan and Bradstreet 1988). P_o is the initial period. P_{contact} is the orbital period that the binary achieves contact.

Astronomical Timescales, Binary Stars

As noted in Part I, Guinan and Bradstreet (1988) is the benchmark paper on the decay of binary star orbits. In that paper, they produce an example plot of the evolution of a detached binary star with a period of 1–5 days into a contact configuration of 0.315 days. This is reproduced here as Figure 2. The aging models in their work are calibrated by the SAC (4.6×10^9 years). The effect of this is seen in the time axis scales of tens of millions to tens of billions of years. Figure 3 (adapted from Guinan, Bradstreet, and Robinson, 1987) shows a graphic depiction of the same process including the final coalescence into a fast-rotating A-type star.

The Age Determination from Observations of Close Binaries Undergoing AML

Using our personal observations of close eclipsing binaries spanning a quarter of a century, Part I presented negatively measured dP/dt 's (rate of period change) of a number of solar-type stars (Samec and Figg, 2012). I assumed that these period changes were due to magnetic braking and the resulting angular momentum loss (AML). Note that the results were *independent* of the usual SAC calibration. Rather that result is dependent only on the NRC chosen in lieu of the SAC; that is, the use of ordinary Keplerian orbital periods. However, due to a calculation error, the results in Part I are underestimated. Although I take a different tack in this paper, a listed retabulation is given in Tables 1–4. In Figure 4, I show a typical O-C residual plot from eclipse timings (O-C means Observed minus Calculated or Predicted by an extant ephemeris; it is the meaning of residual). This type of calculation gives the rate of period decrease of $T = -QE^2 + PE + To$, the standard form of quadratic ephemerides (i.e., the new eclipse happens at time T after so many epochs, or orbits, E , added to the initial eclipse, with a quadratic, Q (“deceleration” term in days/epoch/epoch or d/E^2), and P is the period in days. This acts the same way as a Newtonian kinematical calculation with a deceleration, $y = -\frac{1}{2}at^2 + bt + c$, like the motion of a car with its brakes on. The quadratic term, $-Q$ is $\frac{dP}{dE}$, is the rate of change in period per orbital period (days/Epoch). The relationship of the rate of period change in days/year and $\frac{dP}{dE}$ in days/year is calculated from the formula:

$$\frac{dP}{dE} = \frac{1}{2} \frac{dP}{dt} \cdot \frac{P}{365.24} \quad (1)$$

Part I used AML (angular momentum loss) equations from the analysis of Guinan and Bradstreet (1988). Here L_{orb} is the orbital angular momentum. Using those equations free of the SAC assumptions, equation (2) gives the orbital angular momentum of a gravitationally coupled binary star.

$$L_{orb} = 1.24 \times 10^{52} q(1+q)^{-2} M^{5/3} P^{1/3} \text{ cm}^2 \text{ gm/s} \quad (2)$$

where M is in solar masses.

Taking the derivative, assuming no mass transfer and an insignificant mass loss, the torque, $\mathfrak{T} = \frac{dL}{dt}$, becomes:

$$\frac{dL}{dt} = 4.1 \times 10^{51} q(1+q)^{-2} M^{5/3} P_{orb}^{-2/3} \frac{dP_{orb}}{dt} \text{ cm}^2 \text{ gm/s}^2 \quad (3)$$

where P in days, dP/dt in days/year. Ages, Δt , are calculated from this simple relation

$$\Delta t = \frac{\Delta L}{\mathfrak{T}} \quad (4)$$

In Part I, average values of AML were calculated, neglecting the small changes in mass over the lifetime of the short-period binaries (Maceroni and Rucinski, 2000) and that these binaries begin their life time with periods of 10 days or less (Maceroni

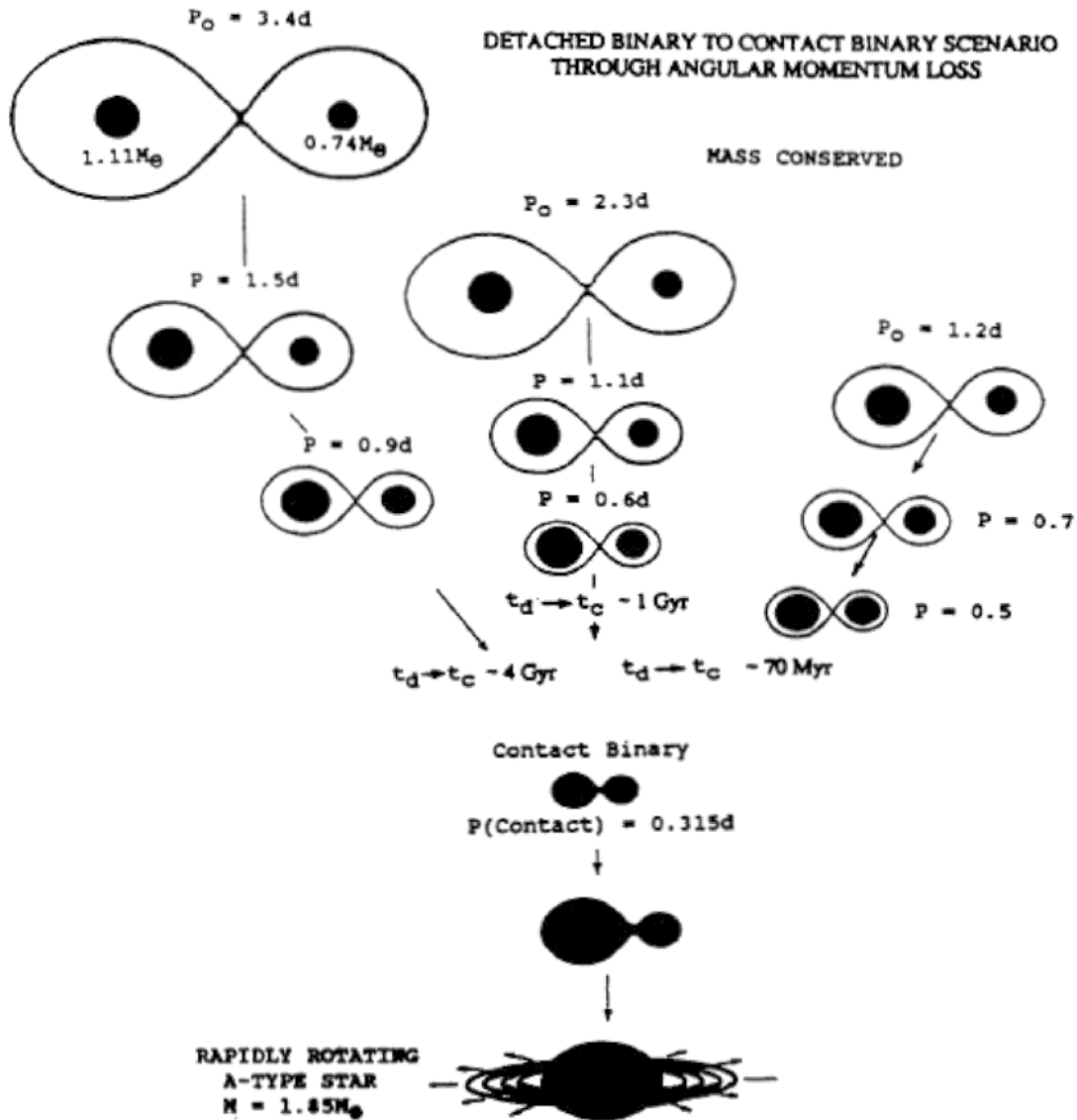


Figure 3. Graphic depiction of the time evolution of a solar-type binary braking from a 1–5 d period binary to a 0.315 period binary and on to a coalesced, rapidly rotating single star (Guinan, Bradstreet, and Robinson, 1987).

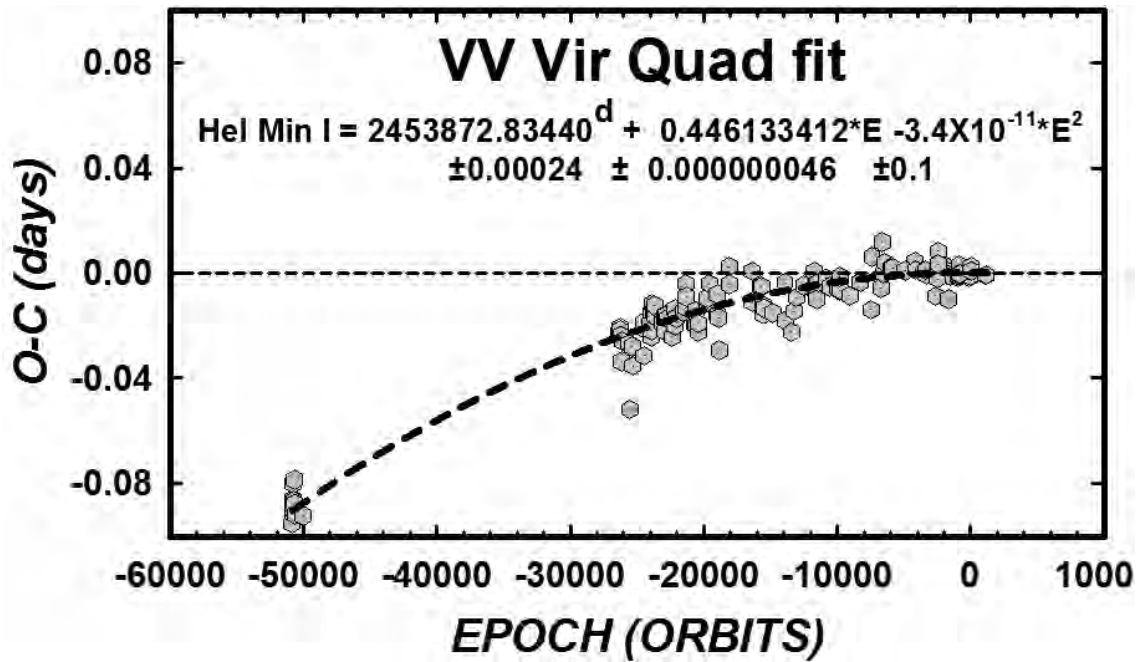


Figure 4. Our observation and calculation from previous eclipse timings shows that the orbit of VV Vir (Samec et al., 2008) is decaying. Since this system is of solar type, I conclude that the period change and the angular momentum loss are negative. I included this binary in our calculation of the age of such binaries.

and Rucinski, 2000; Guinan and Bradstreet, 1988; Kroupa and Burkert, 2001; Henderson and Stassun, 2012).

The Part I table of results included eighteen binaries. Here I correct and update the values from Part I in Tables 1–4. The average apparent ages range from ~25 to 35 million years, only 2–3% of the evolutionary age of the universe for our limited short-period sample. The next section improves on the sample.

A simpler but more accurate tack arises from the fact that the mass ratios used in the tables are not well known unless precision spectroscopic radial velocity curves and their analyses are available. This requirement makes our results questionable. An even simpler approach is possible that does not depend on mass ratios. In this methodology, I use the following equation to make our age calculations,

$$\Delta t = \frac{-\Delta P}{\dot{P}} \quad (5)$$

so that I need only the period and rate of period change. The method only assumes that the chosen systems have a continuous, quadratically decreasing period. ΔP is the difference in the

present orbital period of the binary minus its initial period. The quantity $\dot{P}$ is the rate of change in the period, $\frac{dP}{dt}$, equation (5). In addition, I have spent months surveying the literature and Internet sites, including the American Association of Variable Stars (AAVSO) O-C files created and maintained by Dr. Bob Nelson (AAVSO 2015). I also added additional binaries from my recent studies. The binary star community is indebted to Dr. Nelson's continued work in handling thousands of period studies of eclipsing binary stars. I was able to extend the original 18 systems of Part I to some 124 binaries with periods ranging in orbital periods 0.21 days to 9.3 days.

New Extended Results

I found that the observed rate of angular momentum loss has a much greater effect on the ages of short-period binaries than proposed by the binary-star community. Recently, I have been studying precontact WUMa binaries (Samec et al. 2015, 2014, 2013, 2012a, 2012b); that is, solar-type stars exist in detached (separated) binary stars with periods up to ~10 days. Thus the current study extends to longer periods than usually accorded to close binaries. Due to the inclusion of these longer-period

Table 1. Eratta¹: Results of 25 Years of Observing Solar-Type Binaries AML

	dp/dE (d/E)	dP/dt (d/yr)	period (d)	Est. Spec. Type	M_1 ($M_\odot$)	M_2	M
AK CMi	-5.00E-11	-6.45E-08	0.5658964	A3	2.40	1.56	3.96
AO Cam (14)	-5.69E-11	-1.26E-07	0.3299	G0V	1.20	0.40	1.60
AT Aqr	-3.90E-11	-7.54E-08	0.37802984	G5	0.92	0.33	1.25
BE Cep	-1.60E-11	-2.75E-08	0.42439404	K1	0.77	0.52	1.29
BM UMa	-5.40E-08	-1.45E-04	0.27122032	K3	0.73	0.37	1.10
CN And	-9.80E-11	-1.55E-07	0.46279007	F6	1.30	0.50	1.80
EH Hydra	-1.60E-11	-4.23E-08	0.27663622	G6	0.91	0.29	1.20
EK Com	-2.05E-11	-5.62E-08	0.26668637	K1	0.77	0.24	1.01
GSC 2537 -0520	-1.61E-10	-3.17E-07	0.3710377	G5	0.92	0.15	1.07
HM Mon	-1.80E-11	-3.23E-08	0.4076	G2	1.00	0.59	1.59
V1128 Tau	-3.40E-11	-8.13E-08	0.30537273	G3	1.00	0.51	1.51
V361 Lyr	-3.60E-11	-8.49E-08	0.30961373	F8	1.26	0.87	2.13
V524 Mon	-1.10E-11	-2.83E-08	0.28361604	G8	0.88	0.42	1.30
V803 Aql	-9.00E-11	-2.50E-07	0.26342299	K3	0.73	0.73	1.46
V965 Cyg	-6.50E-11	-7.41E-08	0.64056706	A3	2.45	1.59	4.04
VV CVn	-3.14E-09	-4.30E-06	0.53292205	F2	2.60	1.30	3.90
VV Vir	-3.50E-11	-5.73E-08	0.4461334	G0	1.05	0.45	1.50
XZ Cmi	-3.50E-11	-4.42E-08	0.57880796	F3	1.50	1.25	2.75
Average	-3.22E-09	-8.40E-06	0.395258		1.24	0.67	1.91

¹Replaces Table IVa, Paper 1.

Explanation for Tables 1–4: Tables 1–4 replace Tables 4a, 4b, 5, and 6 respectfully in paper 1. As I state earlier in this paper, “The Part I table of results included eighteen binaries. Here I correct and update the values from paper 1 in Tables 1–4. The average apparent ages range from ~25 to 35 million years, only 2–3% of the evolutionary age of the universe for our limited short-period sample.”

binaries, I have extended our range of initial periods to 20 days. In our results, I assumed 5 days as the birth period for binaries of period 0.2–0.5 days. Further, I assumed a birth period of 8 days for 0.5–0.8-day periods, 10 days for 0.8–1.5-day periods, and 15 and 20 day periods from 1.5–9.3 days.

The results begin in Table 7. The overall average age of our extended sample is about 80 million years. This is only 0.6 % (0.006) of the 13.80-billion-year evolutionary age of the universe. Although this does not equal the oft-cited age of 6000–10,000 years in creation literature, I remind the reader

that this value is the apparent age of a *time-dilated universe*. The earth and, I believe, the entire solar system remains in the range of ages last mentioned. And only some ~100 million years (not 13.80 billion!) years of apparent history is exhibited at least in the nearby (<2 kiloparsec, or about 6000 LY) cosmos—and probably for the “deep” universe as well.

In the example given by Guinan and Bradstreet (1988), shown in Figure 2, using their magnetic-braking equations, which include the SAC, the scenario of a present-contact binary with a 0.315-day period is calculated. The sample calcu-

Table 2. Eratta²: Results, continued

	L ₂ (today)	q=M ₂ /M ₁	dL/dt	L ₁ , 5 d (initial)	L ₁ , 8d (initial)	L ₁ , 10d (initial)
	1.825E+51	0.65	-8.017E+40	1.613E+52	2.580E+52	3.226E+52
	1.450E+50	0.36	-1.228E+38	1.918E+51	3.068E+51	3.835E+51
	2.146E+50	0.68	-9.506E+37	2.528E+51	4.046E+51	5.057E+51
	9.582E+49	0.50	-1.666E+41	1.766E+51	2.826E+51	3.533E+51
	9.548E+49	0.37	-3.093E+38	1.702E+51	2.724E+51	3.405E+51
	3.406E+50	0.39	-1.713E+39	3.680E+51	5.888E+51	7.360E+51
	9.262E+49	0.31	-4.932E+37	1.674E+51	2.678E+51	3.348E+51
	6.600E+49	0.31	-2.693E+37	1.237E+51	1.980E+51	2.475E+51
	7.050E+49	0.17	-1.210E+38	9.500E+50	1.520E+51	1.900E+51
	2.816E+50	0.59	-2.760E+38	3.454E+51	5.527E+51	6.908E+51
	1.868E+50	0.51	-4.824E+38	3.059E+51	4.894E+51	6.118E+51
	3.605E+50	0.69	-3.596E+39	5.822E+51	9.315E+51	1.164E+52
	1.302E+50	0.47	-7.180E+37	2.296E+51	3.673E+51	4.591E+51
	1.691E+50	1.00	-2.189E+39	3.210E+51	5.136E+51	6.420E+51
	2.144E+51	0.65	-7.332E+40	1.674E+52	2.678E+52	3.347E+52
	1.564E+51	0.50	-2.825E+42	1.467E+52	2.348E+52	2.935E+52
	2.521E+50	0.43	-2.771E+38	2.825E+51	4.521E+51	5.651E+51
	1.055E+51	0.83	-7.782E+39	9.114E+51	1.458E+52	1.823E+52
Average	5.050E+50	0.52	-1.757E+41	5.154E+51	5.154E+51	1.031E+52

²Replaces Table IVb, Paper 1.

lation shows the decrease in the orbits over time of 5 different initial periods P_0 from 1d to 5d. It is of interest here that they state that systems having periods $P_0 > 6d$ may not experience this braking effect as main sequence stars since the tidal effects are small due to their relatively large separations, so they cut off their initial period at 5d. Note that all the stars except for two studied here have periods greater than 5d. These systems were selected only on the basis that they appear to be undergoing magnetic braking. Thus, my unwitting selection may lend credibility to their prediction. As shown in the figure, the time to reach contact depends strongly on the initial period. Their calculations yield an age of 17 Gyr (!) for an initial period of 5 days and 30 Myr for $P_0=1d$. In my sample, using binaries with periods from 0.30 to 0.32d, I find, from observational rates of decay that the time to attain contact ranges from 27 to 58 mil-

lion years, averaging 47, nearer to the prediction for initial 1d periods. My result for this transition (braking from a 5d period to 0.32 d) is far short of 17000 million years (17 Gyr). In fact, it is only 0.28% of that age (some 2–3 orders of magnitude)! Binary evolution is taking place at a rate of nearly 400 times that predicted by theory! Using the 5-day limiting period of Guinan and Bradstreet, my sample decreases to 24 binaries, and the age of this group is about 60 million years. This is only 0.4 % (0.004) of the 13.80-billion-year evolutionary age of the universe. So our results remain the same order of magnitude.

Conclusion

The conclusion of this study is that the observable events in the cosmos outside of the solar system really did happen and

Table 3. Eratta³: Time (Years) to Change from 10-, 8-, 5-Day Periods to Present Orbital Periods (Corrected Table)

	Age (years) 5d	Age (years) 8d	Age (years) 10d
	2.83E+07	3.77E+07	4.26E+07
	1.17E+07	1.50E+07	1.68E+07
	2.07E+07	2.68E+07	3.01E+07
	5.95E+07	7.76E+07	8.71E+07
	9.27E+03	1.18E+04	1.32E+04
	1.10E+07	1.44E+07	1.62E+07
	3.22E+07	4.10E+07	4.57E+07
	2.38E+07	3.03E+07	3.38E+07
	4.89E+06	6.32E+06	7.09E+06
	5.00E+07	6.50E+07	7.29E+07
	1.75E+07	2.24E+07	2.50E+07
	1.69E+07	2.16E+07	2.41E+07
	4.86E+07	6.20E+07	6.91E+07
	5.33E+06	6.78E+06	7.55E+06
	2.58E+07	3.46E+07	3.92E+07
	4.16E+05	5.50E+05	6.22E+05
	2.92E+07	3.81E+07	4.29E+07
	4.18E+07	5.56E+07	6.29E+07
Average	2.38E+07	3.09E+07	3.47E+07

³Replaces Table V, Paper 1.

are therefore objects of scientific study for the creation scientist. Phenomena were not just created with *appearance of age*. The events are as follows: The stars were created, and perhaps many coalesced from clouds of gas and lived out their lives and are living out their lives. Normal solar-type stars went through their nuclear burning cycles to become AGB stars, followed by planetary nebula and finally white dwarfs after they spent their nuclear fuels. More massive stars went through their cycles faster, ending their lives as supernovae. Solar-type binaries began their lives as well-detached but orbiting stars, and they slowly decreased in period through magnetic braking as their orbits shrunk. They became semidetached, and then contact binaries that we presently observe. As an aside, but an important note, some astronomers believe that contact binaries are the

Table 4. Eratta⁴: Average, Maximum and Minimum Results (Corrected)

	Age (years)		
	5d Initial Period	8d Initial Period	10d Initial Period
Average	2.38X 10 ⁺⁰⁷	3.09X10 ⁺⁰⁷	3.47X10 ⁺⁰⁷
Maximum	5.95X10 ⁺⁰⁷	7.76X10 ⁺⁰⁷	8.71X10 ⁺⁰⁷
Minimum	4.16X10 ⁺⁰⁵	5.50X10 ⁺⁰⁵	6.22X10 ⁺⁰⁵

⁴Replaces Table VI, Paper 1.

most abundant of all variable stars in the cosmos — indeed, they are very frequent in the heavens! Their abundance conveys a message that should be heeded by the creation community. Finally, judging from the occurrence of very rapidly rotating spotted stars in clusters and in the field, I believe some of the binaries have already merged into single stars. *The occurrence of such objects in the evolutionary view is probably impossible age wise!* They should not exist in a universe of such a “young age” as 13.80 billion years — at least to an evolutionary astronomer.

This paper gives physical confirmation of the youthful age, in a creationary sense, of the universe in a *time-dilation* scenario. As I noted earlier in this article, and as someone has called to our attention at a recent meeting, *much of this prehistory took place during Creation Week following the creation of the first stars on Day 4*. So the event postulated by Humphreys falls into the category of a Creation Week event. Regardless, the phenomena did take place and are *not due to an apparent, ex nihilo, created history*. The events we see truly took place and are objects of legitimate scientific inquiry that the Lord has allowed His children to study. “O give thanks unto the God of heaven: for his mercy endureth for ever” (Psalm 136:26 KJV). “For in six days the LORD made heaven and earth, the sea, and all that in them is, and rested the seventh day: wherefore the LORD blessed the Sabbath day, and hallowed it” (Exodus 20:11 KJV).

Acknowledgments

I and my astronomical collaborators, which include well-known creationists, wish to thank the public and private observatories that I have been allowed use to make this contribution to creation science, and the Creation Research Society for their generous support of this project.

Table 5. Extended Study Including 124 Close Binary Stars

		Ref	dp/dE (d/E)	dP/dt (d/yr)	period (d)	Est. Spec. Type
1	V731 Her	28	-1.34E-10	-4.60E-07	0.2132017	F6
2	CC Com	8, 28	-5.02E-12	-1.66E-08	0.2206861	K4/5
3	V1104 Her	36	-9.28E-12	-2.97E-08	0.2278759	K5
4	RW Tri	21	-2.12E-12	-6.67E-09	0.2318830	G8
5	V579 Lyr	25	-2.92E-10	-8.78E-07	0.2429093	K3
6	V400 Lyra	24,25	-9.08E-11	-2.62E-07	0.2534250	K1
7	V1067 Her	28	-1.89E-10	-5.34E-07	0.2581060	K2
8	V803 Aql	28	-9.00E-11	-2.50E-07	0.2634230	K3
9	EK Com	28,30	-3.29E-11	-9.00E-08	0.2666848	K2
10	V384 Ser	28	-5.55E-11	-1.51E-07	0.2687280	K1
11	BM UMa	33	-2.78439E-11	-7.50E-08	0.2712000	K0V
12	EF CVn	28	-4.63E-11	-1.24E-07	0.2720490	G6
13	EH Hya	28	-1.60E-11	-4.22E-08	0.2766362	G6
14	VW Cep	28	-6.84E-11	-1.80E-07	0.2783101	G5
15	BX Peg	16,28	-4.64E-11	-1.21E-07	0.2804170	G8
16	BL Leo	2	-1.78E-11	-4.61E-08	0.2819207	G5
17	EI CVn	15	-1.20654E-10	-3.11E-07	0.2834000	K5V
18	V524 Mon	28	-1.10E-11	-2.83E-08	0.2836160	G8
19	EP Cep	34	-2.96E-10	-7.46E-07	0.2897391	K1
20	V676 Cen	28	-8.58E-12	-2.14E-08	0.2923940	G6
21	TZ Boo	4	-9.00E-12	-2.21E-08	0.2971599	G1
22	GZ And	28	-2.44E-11	-5.85E-08	0.3050165	K5
23	V1128 Tau	28	-3.40E-11	-8.13E-08	0.3053727	G3
24	AV Crb	28	-9.55E-11	-2.26E-07	0.3081900	K1
25	V361 Lyr	28	-4.50E-11	-1.06E-07	0.3096121	F8
26	HR Boo	28	-7.4E-11	-1.71E-07	0.3159669	G6
27	TY Boo	28,35	-7.81E-12	-1.80E-08	0.3171484	G8
28	BO Aur	28	-9.78E-11	-2.25E-07	0.3181935	M2
29	V1115 Cas	28	-3.81E-10	-8.61E-07	0.3232785	K2
30	TU Boo	28	-4.31E-11	-9.70E-08	0.3242870	G3
31	V369 Cep	34	-6.94E-11	-1.54E-07	0.3281891	K1
32	AO Cam	14	-5.69E-11	-1.26E-07	0.3299000	G0V
33	AH Tau	14	-3.18809E-11	-7.00E-08	0.3327000	G1
34	AQ Boo	28	-8.09E-11	-1.77E-07	0.3331376	F2
35	EQ Tau	20	-1.06E-11	-2.27E-08	0.3413485	G0
36	BY Peg	20	-1.18E-10	-2.51E-07	0.3419380	K3

Table 5. Extended Study Including 124 Close Binary Stars

		Ref	dp/dE (d/E)	dP/dt (d/yr)	period (d)	Est. Spec. Type
37	VW Boo	6	-6.81E-11	-1.45E-07	0.3423155	G5
38	ES Cep	34	-5.06E-11	-1.08E-07	0.3424552	M0
39	V781 Tau	28	-2.25E-11	-4.77E-08	0.3440983	G0
40	GR Vir	10	-2.05E-10	-4.32E-07	0.3469788	F9-G0
41	KN Vul	28	-1.1522E-10	-2.36E-07	0.3573325	G0
42	VZ Lib	28	-1.71E-04	-3.49E-01	0.3582550	G2
43	GSC 0883-1116	28	-7.00E-10	-1.41E-06	0.3636090	F0
44	GV Boo	28	-6.83E-10	-1.36E-06	0.3678660	G8
45	GSC 3108-0057	28	-1.94E-10	-3.84E-07	0.3687510	G6
46	V417 Aql	28	-2.36E-10	-4.65E-07	0.3703180	G2
47	GSC 2537-0520	28	-1.61E-10	-3.17E-07	0.3710377	G5
48	U Peg	28	-6.06E-11	-1.18E-07	0.3747797	F3
49	AT Aqr	28	-3.90E-11	-7.54E-08	0.3780298	G5
50	AD Phe	28	-6.94E-11	-1.33E-07	0.3799210	G8
51	V1094 Her	28	-7.52E-10	-1.40E-06	0.3921114	G3
52	V356 Mon	5	-4.65E-11	-8.57E-08	0.3963413	F9
53	V2240 Cyg	28	-1.02E-09	-1.84E-06	0.4041940	F3
54	GSC3208-1986	28	-7E-10	-1.26E-06	0.4045659	F3V
55	SS Ari	11	-2.13E-10	-3.83E-07	0.4059940	F8
56	HM Mon	28	-1.80E-11	-3.23E-08	0.4076000	G2
57	DE Lyn	28	-3.15E-10	-5.63E-07	0.4088170	G6
58	CU Tau	9	-1.02E-09	-1.81E-06	0.4125378	G0
59	V1095 Her	28	-2.88E-10	-5.07E-07	0.4153750	K5
60	WZ Cep	7, 28	-2.12E-10	-3.71E-07	0.4174409	F7
61	EH Cnc	28	-1.77E-10	-3.10E-07	0.4180321	F3
62	BE Cep	28	-2.15E-11	-3.71E-08	0.4243978	K1
63	AP Leo	28	-6.38E-11	-1.08E-07	0.4303572	G0
64	AW UMa	28	-6.023E-11	-1.00E-07	0.4387249	F0
65	BS Cas	28	-1.70E-10	-2.82E-07	0.4404632	G5V
66	TV Mus	9	-1.32E-10	-2.16E-07	0.4456794	G0-G1
67	VV Vir	28	-3.50E-11	-5.73E-08	0.4461334	G0
68	V502 Oph	28	-9.83E-11	-1.58E-07	0.4533908	F9
69	CN And	28,32	-9.80E-11	-1.55E-07	0.4627901	F6
70	V653 Lyr	28	-3.58E-10	-5.57E-07	0.4688106	F6
71	FT Lup	28	-1.17E-10	-1.82E-07	0.4700790	F5
72	II Per	28	-4.514E-11	-6.87E-08	0.4798500	K2V

Table 5. Extended Study Including 124 Close Binary Stars

		Ref	dp/dE (d/E)	dP/dt (d/yr)	period (d)	Est. Spec. Type
73	TT Cet	28	-3.97E-11	-5.98E-08	0.4859530	F6
74	GSC 2038-0293	28	-3.43E-10	-5.06E-07	0.4954110	K3
75	V724 Aql	20	-3.49E-11	-4.93E-08	0.5175994	F7
76	RU UMi	18	-7.186E-11	-1.00E-07	0.5249259	F1
77	V878 Her	28	-1.341E-10	-1.85E-07	0.5294733	F8
78	VV CVn	28	-3.14E-09	-4.30E-06	0.5329221	F2
79	AK CMi	28	-5.00E-11	-6.45E-08	0.5658964	A3
80	V530 And	28	-1.40E-08	-1.77E-05	0.5771072	F4V
81	DF Lyr	28	-7.73E-11	-9.78E-08	0.5771280	F8
82	XZ CMi	28	-3.50E-11	-4.42E-08	0.5788080	F3
83	WZ Cyg	28	-6.26E-11	-7.83E-08	0.5844680	K0
84	GSC4968-0725	28	-1.00E-08	-1.23E-05	0.5962390	K0
85	RS Ser	28	-1.12E-10	-1.37E-07	0.5981380	F8
86	CC Peg	28	-4.45E-12	-5.37E-09	0.6055974	F5
87	BX And	31	-1.03E-10	-1.23E-07	0.6101101	F4
88	EG Cas	28	-1.60E-10	-1.91E-07	0.6114435	A4
89	ZZ Cyg	28	-1.07E-10	-1.25E-07	0.6286163	F6
90	RU Eri	13	-1.90E-12	-2.20E-09	0.6321987	F3V
91	V965 Cyg	28	-6.50E-11	-7.41E-08	0.6405671	A3
92	V0355 Vir	28	-3.00E-08	-3.34E-05	0.6555290	K5
93	IK Per	28	-2.33E-10	-2.52E-07	0.6760347	A2
94	IR Cas	1	-1.19E-10	-1.28E-07	0.6806860	F4
95	V104 Cyg	28	-1.64E-10	-1.74E-07	0.6856900	G4
96	CU Hya	28	-1.343E-09	-1.36E-06	0.7190649	F6
97	CN Com	28	-1.79E-10	-1.78E-07	0.7354410	K0
98	AW Cam	28	-2.67E-11	-2.53E-08	0.7713460	A0
99	DZ Cas	3	-9.88E-11	-9.20E-08	0.7848864	A9
100	RT Per	12	-1.08E-10	-9.29E-08	0.8494069	F5-G0
101	VW CVn	28	-5.17E-09	-4.44E-06	0.8499056	A4
102	RR Lyr	28	-7.61E-11	-6.07E-08	0.9154230	F5
103	NZ Per	28	-1.56E-09	-1.22E-06	0.9379200	G2
104	V501 Oph	28	-5.49E-11	-4.15E-08	0.9679500	F4
105	X Tri	19	-1.89E-10	-1.42E-07	0.9715397	A2/G3
106	CV Cyg	28	-5.6384E-10	-4.19E-07	0.9834178	FGIII
107	V346 Aql	28	-8.06E-11	-5.32E-08	1.1063625	A0
108	XZ Per	28	-4.32E-10	-2.74E-07	1.1516210	G0

Table 5. Extended Study Including 124 Close Binary Stars

		Ref	dp/dE (d/E)	dP/dt (d/yr)	period (d)	Est. Spec. Type
109	YZ CVn	28	-1.01E-10	-6.30E-08	1.1755540	G1
110	IM Aur	28	-4.95E-10	-2.90E-07	1.2472866	K0
111	GS Boo	28	-5.61E-09	-3.26E-06	1.2567870	G0
112	GSC 0262-0948	28	-1.30E-08	-6.95E-06	1.3714155	G8
113	W UMi	28	-1.00E-09	-4.29E-07	1.7011576	A3
114	RW Mon	28	-6.40E-10	-2.45E-07	1.9060910	A0
115	V640 Ori	28	-1.55E-09	-5.61E-07	2.0227500	F7
116	CW Peg	21,22,28	-5.29E-09	-1.63E-06	2.3725133	A2
117	TX UMa	12	-2.99E-09	-7.13E-07	3.0632881	B8V,G0 III-IV
118	TY Peg	28	-4.93E-10	-1.16E-07	3.0922550	A2/G
119	PX Cep	28	-1.36E-08	-3.17E-06	3.1268280	F8
120	RY UMi	28	-2.51E-08	-5.62E-06	3.2648140	K2
121	WY Per	28	-3.41E-08	-7.50E-06	3.3270300	F2
122	Y Psc	28	-4.78E-09	-9.26E-07	3.7700000	A5
123	RT Lac	28	-3.96E-08	-5.70E-06	5.0737202	G5
124	RY Gem	28	-8.31E-08	-6.52E-06	9.3002990	A2

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Table 6. Estimates of the “Apparent Age” of the Universe

P0 5d (initial)	Po, 8d (initial)	Po, 10d (initial)	Po 15d (initial)	Po 20d (initial)
1.04E+07	1.69E+07	2.13E+07	3.21E+07	4.30E+07
2.88E+08	4.68E+08	5.88E+08	8.89E+08	1.19E+09
1.61E+08	2.61E+08	3.29E+08	4.97E+08	6.65E+08
7.15E+08	1.16E+09	1.46E+09	2.21E+09	2.96E+09
5.42E+06	8.84E+06	1.11E+07	1.68E+07	2.25E+07
1.81E+07	2.96E+07	3.72E+07	5.64E+07	7.55E+07
8.88E+06	1.45E+07	1.82E+07	2.76E+07	3.70E+07
1.90E+07	3.10E+07	3.90E+07	5.90E+07	7.91E+07
5.26E+07	8.59E+07	1.08E+08	1.64E+08	2.19E+08
3.13E+07	5.12E+07	6.45E+07	9.76E+07	1.31E+08
6.31E+07	1.03E+08	1.30E+08	1.96E+08	2.63E+08
3.81E+07	6.22E+07	7.83E+07	1.19E+08	1.59E+08
1.12E+08	1.83E+08	2.30E+08	3.48E+08	4.67E+08
2.63E+07	4.30E+07	5.41E+07	8.20E+07	1.10E+08
3.91E+07	6.39E+07	8.05E+07	1.22E+08	1.63E+08
1.02E+08	1.67E+08	2.11E+08	3.19E+08	4.28E+08
1.52E+07	2.48E+07	3.12E+07	4.73E+07	6.34E+07
1.66E+08	2.72E+08	3.43E+08	5.19E+08	6.96E+08
6.31E+06	1.03E+07	1.30E+07	1.97E+07	2.64E+07
2.20E+08	3.60E+08	4.53E+08	6.86E+08	9.20E+08
2.13E+08	3.48E+08	4.39E+08	6.65E+08	8.91E+08
8.03E+07	1.32E+08	1.66E+08	2.51E+08	3.37E+08
5.77E+07	9.46E+07	1.19E+08	1.81E+08	2.42E+08
2.07E+07	3.40E+07	4.28E+07	6.49E+07	8.70E+07
4.42E+07	7.24E+07	9.13E+07	1.38E+08	1.85E+08
2.74E+07	4.49E+07	5.66E+07	8.58E+07	1.15E+08
2.60E+08	4.27E+08	5.38E+08	8.16E+08	1.09E+09
2.08E+07	3.42E+07	4.31E+07	6.54E+07	8.76E+07
5.43E+06	8.92E+06	1.12E+07	1.71E+07	2.29E+07
4.82E+07	7.91E+07	9.98E+07	1.51E+08	2.03E+08
3.02E+07	4.97E+07	6.26E+07	9.50E+07	1.27E+08
3.71E+07	6.09E+07	7.67E+07	1.16E+08	1.56E+08
6.67E+07	1.10E+08	1.38E+08	2.10E+08	2.81E+08
2.63E+07	4.32E+07	5.45E+07	8.26E+07	1.11E+08
2.05E+08	3.38E+08	4.26E+08	6.46E+08	8.67E+08
1.85E+07	3.05E+07	3.84E+07	5.83E+07	7.82E+07
3.20E+07	5.27E+07	6.64E+07	1.01E+08	1.35E+08
4.32E+07	7.09E+07	8.95E+07	1.36E+08	1.82E+08

Table 6. Estimates of the “Apparent Age” of the Universe

P0 5d (initial)	Po, 8d (initial)	Po, 10d (initial)	Po 15d (initial)	Po 20d (initial)
9.76E+07	1.60E+08	2.02E+08	3.07E+08	4.12E+08
1.08E+07	1.77E+07	2.24E+07	3.40E+07	4.55E+07
1.97E+07	3.24E+07	4.09E+07	6.22E+07	8.34E+07
1.33E+01	2.19E+01	2.76E+01	4.20E+01	5.63E+01
3.30E+06	5.43E+06	6.85E+06	1.04E+07	1.40E+07
3.42E+06	5.63E+06	7.11E+06	1.08E+07	1.45E+07
1.21E+07	1.99E+07	2.51E+07	3.81E+07	5.11E+07
9.96E+06	1.64E+07	2.07E+07	3.15E+07	4.22E+07
1.46E+07	2.41E+07	3.04E+07	4.62E+07	6.19E+07
3.92E+07	6.46E+07	8.15E+07	1.24E+08	1.66E+08
6.13E+07	1.01E+08	1.28E+08	1.94E+08	2.60E+08
3.46E+07	5.71E+07	7.21E+07	1.10E+08	1.47E+08
3.29E+06	5.43E+06	6.86E+06	1.04E+07	1.40E+07
5.37E+07	8.87E+07	1.12E+08	1.70E+08	2.29E+08
2.50E+06	4.13E+06	5.22E+06	7.93E+06	1.07E+07
3.64E+06	6.01E+06	7.59E+06	1.15E+07	1.55E+07
1.20E+07	1.98E+07	2.51E+07	3.81E+07	5.12E+07
1.42E+08	2.35E+08	2.97E+08	4.52E+08	6.07E+08
8.16E+06	1.35E+07	1.70E+07	2.59E+07	3.48E+07
2.53E+06	4.19E+06	5.30E+06	8.06E+06	1.08E+07
9.04E+06	1.50E+07	1.89E+07	2.88E+07	3.86E+07
1.23E+07	2.04E+07	2.58E+07	3.93E+07	5.28E+07
1.48E+07	2.45E+07	3.09E+07	4.71E+07	6.32E+07
1.23E+08	2.04E+08	2.58E+08	3.93E+08	5.28E+08
4.22E+07	6.99E+07	8.84E+07	1.35E+08	1.81E+08
4.55E+07	7.54E+07	9.53E+07	1.45E+08	1.95E+08
1.62E+07	2.68E+07	3.39E+07	5.16E+07	6.94E+07
2.11E+07	3.49E+07	4.42E+07	6.73E+07	9.04E+07
7.95E+07	1.32E+08	1.67E+08	2.54E+08	3.41E+08
2.87E+07	4.76E+07	6.03E+07	9.18E+07	1.23E+08
2.93E+07	4.87E+07	6.17E+07	9.40E+07	1.26E+08
8.13E+06	1.35E+07	1.71E+07	2.61E+07	3.51E+07
2.49E+07	4.15E+07	5.25E+07	8.00E+07	1.08E+08
6.58E+07	1.09E+08	1.39E+08	2.11E+08	2.84E+08
7.55E+07	1.26E+08	1.59E+08	2.43E+08	3.27E+08
8.91E+06	1.48E+07	1.88E+07	2.87E+07	3.86E+07
9.10E+07	1.52E+08	1.93E+08	2.94E+08	3.96E+08
4.48E+07	7.48E+07	9.48E+07	1.45E+08	1.95E+08

Table 6. Estimates of the “Apparent Age” of the Universe

P0 5d (initial)	Po, 8d (initial)	Po, 10d (initial)	Po 15d (initial)	Po 20d (initial)
2.42E+07	4.04E+07	5.12E+07	7.82E+07	1.05E+08
1.04E+06	1.74E+06	2.20E+06	3.36E+06	4.52E+06
6.87E+07	1.15E+08	1.46E+08	2.24E+08	3.01E+08
2.50E+05	4.19E+05	5.32E+05	8.14E+05	1.10E+06
4.52E+07	7.59E+07	9.63E+07	1.47E+08	1.99E+08
1.00E+08	1.68E+08	2.13E+08	3.26E+08	4.40E+08
5.64E+07	9.48E+07	1.20E+08	1.84E+08	2.48E+08
3.59E+05	6.04E+05	7.68E+05	1.18E+06	1.58E+06
3.21E+07	5.40E+07	6.86E+07	1.05E+08	1.42E+08
8.18E+08	1.38E+09	1.75E+09	2.68E+09	3.61E+09
3.57E+07	6.01E+07	7.63E+07	1.17E+08	1.58E+08
2.30E+07	3.87E+07	4.92E+07	7.53E+07	1.02E+08
3.51E+07	5.91E+07	7.52E+07	1.15E+08	1.55E+08
1.99E+09	3.36E+09	4.27E+09	6.54E+09	8.82E+09
5.88E+07	9.93E+07	1.26E+08	1.94E+08	2.61E+08
1.30E+05	2.20E+05	2.80E+05	4.29E+05	5.79E+05
1.72E+07	2.91E+07	3.70E+07	5.69E+07	7.68E+07
3.37E+07	5.72E+07	7.28E+07	1.12E+08	1.51E+08
2.48E+07	4.20E+07	5.34E+07	8.21E+07	1.11E+08
3.14E+06	5.34E+06	6.80E+06	1.05E+07	1.41E+07
2.39E+07	4.08E+07	5.20E+07	8.01E+07	1.08E+08
1.67E+08	2.86E+08	3.65E+08	5.63E+08	7.61E+08
4.58E+07	7.84E+07	1.00E+08	1.55E+08	2.09E+08
4.47E+07	7.70E+07	9.85E+07	1.52E+08	2.06E+08
9.34E+05	1.61E+06	2.06E+06	3.18E+06	4.31E+06

Table 6. Estimates of the “Apparent Age” of the Universe

	P0 5d (initial)	Po, 8d (initial)	Po, 10d (initial)	Po 15d (initial)	Po 20d (initial)
	6.72E+07	1.17E+08	1.50E+08	2.32E+08	3.14E+08
	3.33E+06	5.80E+06	7.44E+06	1.15E+07	1.56E+07
	9.73E+07	1.70E+08	2.18E+08	3.39E+08	4.59E+08
	2.83E+07	4.95E+07	6.35E+07	9.87E+07	1.34E+08
	9.59E+06	1.68E+07	2.15E+07	3.35E+07	4.54E+07
	7.31E+07	1.29E+08	1.67E+08	2.61E+08	3.55E+08
	1.40E+07	2.50E+07	3.23E+07	5.05E+07	6.88E+07
	6.07E+07	1.08E+08	1.40E+08	2.19E+08	2.99E+08
	1.29E+07	2.33E+07	3.02E+07	4.74E+07	6.46E+07
	1.15E+06	2.07E+06	2.68E+06	4.21E+06	5.74E+06
	5.22E+05	9.54E+05	1.24E+06	1.96E+06	2.68E+06
	7.68E+06	1.47E+07	1.93E+07	3.10E+07	4.26E+07
	1.26E+07	2.49E+07	3.30E+07	5.34E+07	7.38E+07
	5.31E+06	1.07E+07	1.42E+07	2.31E+07	3.21E+07
	1.61E+06	3.45E+06	4.68E+06	7.75E+06	1.08E+07
	2.72E+06	6.92E+06	9.73E+06	1.67E+07	2.38E+07
	1.64E+07	4.21E+07	5.93E+07	1.02E+08	1.45E+08
	5.91E+05	1.54E+06	2.17E+06	3.75E+06	5.32E+06
	3.09E+05	8.42E+05	1.20E+06	2.09E+06	2.98E+06
	2.23E+05	6.23E+05	8.90E+05	1.56E+06	2.22E+06
	1.33E+06	4.57E+06	6.73E+06	1.21E+07	1.75E+07
		5.13E+05	8.64E+05	1.74E+06	2.62E+06
			1.07E+05	8.74E+05	1.64E+06
Years	7.11E+07	1.18E+08	1.48E+08	2.26E+08	3.04E+08

Table 7. Time (years) to Change from 20-, 15-, 10-, 8-, 5-day Birth Periods to Present Orbital Periods (See Text)

	P ₀ 5d (initial)	P ₀ , 8d (initial)	P ₀ , 10d (initial)	P ₀ 15d (initial)	P ₀ 20d (initial)	Average	
AGE (Years)	6.05E+07	2.52E+08	6.65E+07	2.14E+07	2.44E+07	8.41E+07	Average
Maximum	7.15E+08	3.36E+09	1.67E+08	1.02E+08	1.45E+08	3.36E+09	MAX
Minimum	1.33E+01	2.20E+05	1.24E+06	8.74E+05	1.64E+06	1.33E+01	MIN
% age of Universe	0.4	1.8	0.5	0.2	0.2	0.6	

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Conference Reports

CRS Conference Abstracts

July 28–30, 2016 • Ann Arbor, MI

On July 28–30, 2016, the Creation Research Society held its sixth conference on the campus of Concordia University in Ann Arbor, Michigan. There were nearly 130 Society members in attendance. The purpose of our meetings is to promote ongoing research, give people an opportunity to gain exposure for their work, and solicit feedback crucial in developing their ideas. We expect that many of these eventually will be published in the Quarterly or some other publication. Since these are works in progress, we normally do not record the presentations. However, we do publish the abstracts provided by the authors. Below are the abstracts of presentations at the 2016 meeting.

*Coordinating Committee:
Kevin Anderson, Bob Hill, and Danny Faulkner*

Plenary Presentations:

The Origin of Information **Gary Locklair**

How can we formalize the obvious implications of informatics (the science of information)? While the fact that information can come only from intelligent agency is obvious, a rigorous formalization of this important evidence for creation is either lacking or communicated poorly.

Informatics should not be confused with the “information theory” concept attributed to Claude Shannon in the

mid-twentieth century. Shannon’s information theory is incomplete and misleading in the context of origins. We need to focus on the concept of information origin, and not just information transmission (as Shannon did).

A good description of the term “informatics” is that it broadly describes the study and practice of creating, storing, locating, manipulating, and sharing information.

Naturalists assert that the creation model misunderstands the central issue and that genetic information can increase over time via materialistic processes. However, what needs to be focused on is the origin of information and not whether preexisting information can generate information. I have no interest in debating materialists who wish to ignore the fundamental question of the origin of

information by citing “just so” stories that indicate information can be generated from preexisting information, or that information content can be increased based upon preexisting information.

Many creationary scientists have investigated and written about the importance of information in the discussion on origins. Perhaps we can get some insight by investigating and researching different arenas. Let’s discuss how mathematics and philosophy can be brought to bear as we formalize informatics to demonstrate that intelligence is necessary to create information.

Megasequences, Ecological Zonation, and the Fossil Record: A Tale of Two Continents

Tim Clarey

The six Sloss sedimentary megasequences have been mapped, correlated, and compiled across North America and Africa, including the Middle East. Stratigraphic information from oil wells, cores, seismic profiles, and measured outcrops were incorporated into our database. Results show a near simultaneous, chapter-by-chapter progression of the Flood across both continents. Deposition was found to begin at the same stratigraphic interval and reached the same maximum coverage level on both continents. The onset of significant Flood deposition began with the Sauk megasequence (consisting of the Cambrian and Lower Ordovician Systems), which initially deposited a blanketlike sandstone across North America, North Africa, and the Middle East. However, the earliest Flood sediments, corresponding to the first three megasequences, were thinner and exhibited less coverage of the continents compared to later megasequences. In addition, the first three megasequences contain almost exclusively shallow marine fossils with very few terrestrial representatives. Later megasequences (Absaroka and Zuni) were both thicker and more extensive on both continents. The Zuni megasequence (Middle Jurassic-Upper Cretaceous) recorded the maximum coverage level and the greatest sedimentary volume and likely corresponds to the high point of the Flood (Day 150). The last megasequence, the Tejas, appears to be the receding phase of the Flood (Days 151–371). These later megasequences contain both terrestrial and marine fossils. The patterns exhibited by the megasequences and the fossils they contain are best explained by an ecological zonation model. Pre-Flood highs and lows were interpreted from the thickness patterns of the megasequences and their respective fossils.

Presentation Abstracts:

How to Reconstruct the Original Genomes of Adam and Eve

Rob Carter

Given a straightforward reading of biblical history, all of humanity should descend from a single man and a single woman who lived around six thousand years ago. With this in mind, we can ask a simple question: What would it take to model the original two genomes? Or, going in the other direction, if we take into account the number of generations, appropriate mutation rates, and estimates of the rate of chromosomal recombination and gene conversion, can we explain modern human genetic diversity starting from that initial couple? The answer to this is a decisive yes. Thousands of complete human genomes are now available from people across the world, and so we have the data we need. Yet several difficulties still stand in our way. The data sets are too large to work with on a home computer, data quality is an ongoing concern, and the data themselves have been collected with known evolutionary biases. But despite this, the fact remains that there is but one human male and female ancestor for the entire world population, there has been a single dispersal of people across the globe, humanity came from a small initial population size, and we experienced a period of incredible population growth that led to a peculiar pattern of ancestry best explained by a Creation/Flood/Babel model.

The Peleg Problem, Part 1: When Did the Event Described in Genesis 10:25 Occur?

Lee Anderson

In their interpretation of Genesis 10:25 (cf. 1 Chronicles 1:19), notable modern biblical creationists have followed the lead of Josephus and Pseudo-Manetho in maintaining that the event described in the biblical text occurred at or near the time of the birth of Peleg. However, lexical analysis of the Hebrew קִנְיָיו (“in his days”) suggests there is a greater likelihood that the temporal referent is to the time of Peleg’s prominence, that is, within the span of his adult years (cf. 1 Kings 16:34; 21:29; 2 Kings 8:20; 23:29; 24:1; 1 Chronicles 22:9; 2 Chronicles 13:23; 21:8; Psalm 72:7; Jeremiah 22:30; 23:6). In this analysis, primary attention is given to examining other occurrences of the lexical form appearing in Genesis 10:25 (i.e., כּ preposition + יָם [masculine plural construct] + 3rd person masculine singular suffix); however, other forms also are considered (e.g., forms without the prefixed preposition, forms with alternative suffixes, etc.). In response to anticipated objections about the

reasonableness of Peleg's name bearing a connection to an event occurring in his adult life, this study also surveys Old Testament naming conventions, with special attention given to those in the Mosaic corpus (e.g., Genesis 3:20; 4:25, 26; 5:29; 16:15; 17:5; 21:3; etc.), and finds the presentation of Peleg's name in Genesis 10:25 at variance stylistically from the general pattern observed. Accordingly, this study tentatively concludes there is a credible textual basis for asserting that the event noted in Genesis 10:25 occurred later in the lifetime of Peleg than is commonly argued.

The Peleg Problem, Part 2: What Was the Event Described in Genesis 10:25?

Lee Anderson

Modern biblical creationists tend toward seeing נִפְלְגָה הָאֶרֶץ ("the earth was divided") in Genesis 10:25 (cf. 1 Chronicles 1:19) as a reference either to the linguistic confusion occurring at Babel and subsequent scattering of the human populace, or to a geologic breakup of the continental landmass. However, there are problems with each of these views, as is summarily demonstrated in this study. Building on discussions by Robert Davidson, Bruce Vawter, S. D. Walters, Nahum Sarna, David Fouts, and others, this study proposes instead that Genesis 10:25 refers to the physical division of land by means of irrigation canals. Support for this perspective derives from analysis of the relevant lexical data (פִּלַּג in Hebrew, and cognates in both Akkadian and Ugaritic), assessment of the usage of both the nominal and verbal forms in other biblical passages (especially in Job 38:25; cf. Job 29:6; Psalms 1:3; 46:5; 55:10; 65:10; 119:136; Proverbs 5:16; 21:1; Isaiah 30:25; 32:2; Lamentations 3:48), and consideration of the broader context of segmented genealogies in Genesis. Intertwined with the consideration of contextual evidence are critical observations on the polemical angle of Genesis 10:25 in the face of the relevant ancient Near Eastern literature (namely *Atra-ḫašs*). This study tentatively concludes that Genesis 10:25 refers to the canaling of the land in order to advance Genesis's theological view of mankind made in the image of God (Genesis 1:26–27; 9:6) and so being a capable innovator (cf. Genesis 4:20–22), rather than being helplessly dependent on the gods for cultural advancement.

Helminths, the Microbiome, and the Microbe Interface System

Frank Sherwin

Parasitology is first and foremost an ecological science regarding the parasite, host, and environmental factors—

both macro and microscopic. Interfaces help autonomous entities, like humans, microbes, and helminths, exchange information and material. Design analysis anticipates that an innate interface system fully controls the harmony between humans and microbes. The multifunctional "microbe interface system" (MIS) is the key link associating us to the microbiome and, it is suggested, helminths. In the pre-Fall world, could the microbiome be extended to mutualistic helminths forming dynamic host system-to-metazoan relationships? There are echoes of this relationship today with increasing evidence that some parasitic helminths are either neutral or even beneficial. Helminth infection counters IBD by activating the microbe interface system response that changes the microbiome. Lab animals chronically infected with helminths produced increased levels of short-chain fatty acids produced by the microbiome, activating a family of receptors that in turn influence the microbe interface system. Clearly, there is a link between the microbiome, helminth infection, and the immune system/MIS. Many creation zoologists see parasites as creatures originally intended for health in God's very good creation. They existed in a truly mutualistic relationship between worm and man. A naturally beneficial symbiotic relationship could have played major roles in organism-microbiome interactions in the pre-Fall world (indeed, the microbiome has been recently described as revealing remarkably more harmony than antagonism in organism-microbiome relationships). Non-self-internal creatures communicated with the host's interface-distinctive elements (immune system), while others were free-living (e.g. *Strongyloides*). After the Fall, some became parasitic with a deleterious biology (e.g., malaria, *Naegleria*, schistosomiasis, etc.). The Curse (Genesis 3) may have involved minor adjustments to existing structures and/or the relaxation of controls resulting in a chaotic ecology including devastating parasitic infections. As with viruses, biological research was somewhat stymied with the quaint idea that all parasites are bad, but design analysis can identify such naturalistic biases. Although we live in a tainted, post-Fall world, more promising and useful research can be expected from the study of created features in the microbe interface system, the key link associating us to trillions of microbes and macroscopic creatures.

Stratigraphy and the Flood. What Is Sure, What Isn't, and Where to Go from Here

Nathan Mogk

Stratigraphy is the basis for interpretation of geological evidence, as the means by which observations are categorized and communicated. What if the simple act of categorization,

often equated with the evidence itself, were far from certain? In line with the biblical call to examine everything carefully, I provide an analysis of stratigraphic methods defined in the North American Stratigraphic Code (NASC). Using conceptual examples, I highlight limitations and cautions about each method, summarize relevant creationist developments, and provide recommendations for usage in the creationist geological practice.

Although stratigraphic categorizations are largely based on geometrical and other physical characteristics, the significance, particularly temporal, of the observations is determined subjectively. Because of this, and because the dynamic nature of the Flood potentially limits the applicability of the foundational principles of stratigraphic practice, such as the “law” of superposition, creationists should be careful to understand the methods of naturalistic studies before relying on their stratigraphic interpretations. In particular, there is no stratigraphic method that provides global temporal correlations, like the Uniformitarian Chronostratigraphic Column (UC), in a creationist synthesis.

Genomic and Baraminological Analysis of Nucleocytoplasmic Large DNA Viruses

Matthew Cserhati

According to evolutionist Jean-Michel Claverie, “The disturbing fact that most virus genes might not have originated from one of today’s three cellular domains only helps revive the spectrum of intelligent design.”

The large-sized genomes and unique gene content of nucleocytoplasmic large DNA viruses (NCLDV or girus) have become the focus of attention in recent research. Some evolutionists claim with much fanfare that these viruses form a new “fourth domain” of life besides eukaryotes, bacteria, and archaea. They believe them to be the ancestor of the eukaryotic nucleus and that they harbor genes from eukaryotes, bacteria, and archaea through horizontal gene transfer, thereby facilitating genomic evolution.

Evolutionists delineate ~50 core genes with varying distribution in the genomes of 7 NCLDV families, purportedly demonstrating their monophyly. Upon closer examination this is not warranted, since only 14 of these genes are unique to NCLDVs.

NCLDVs also contain a high ratio of ORFan genes, without homologs in other species, supporting their independent creation apart from other organisms. This ORF ratio remains high despite newer species being discovered and newer sequences added to the major sequence databases. We found that for the 49 NCLDV species in the COG database, on average 74.6% of their proteins were ORFans. The

common protein content between all possible species pairs were compared, and based on Jaccard-coefficient values, 10 NCLDV baramins were predicted, with 2–8 members each. Some evidence exists in the scientific literature showing that NCLDVs undergo rapid genome decay and genomic variation unexpected by evolutionary theory.

The “Unnatural” Mass of the Higgs Boson Creates a “Nightmare Scenario” for Theoretical Physicists

Mary Beth De Repentigny

The Higgs boson has been discovered at the Large Hadron Collider with a determined mass of 125 billion electron volts. This low Higgs mass exhibits extreme fine-tuning in the parameters of the universe for life as we know it, leaving the proponents of the big bang theory struggling to find a naturalistic explanation. There has been no evidence coming out of the LHC supporting any of the theories previously proposed to explain this preposterous “mass hierarchy problem”—including the much touted “supersymmetry.” We will explore the ramifications of the discovery of a low Higgs mass and the ways in which the adherents of Darwinian philosophy try to theorize their way out of what to them has been called the “nightmare scenario.” Apparently, finding a finely tuned Higgs mass is frightening to them because of the anthropic implications of this amazing evidence for an intelligent Creator.

Biological Algorithms: The Failure of Gradual Evolution

Adrian Chira

Gradualism is one of the tenets of Darwinism, touted to explain complexity. However, it assumes that all biology has the same nature observed in microevolution, which is argued is false so that the extrapolation fails. From computer code, man-made products to natural processes and biology, there is a virtually universal distinction between parts with properties and algorithmic functions that coordinate them. This was acknowledged by Darwin in chapter 7 of *Origins* but was then mostly ignored. It was revived “recently” by systems biology, but its implications for DNA and evolution have been largely unexplored. Further, Darwinists have missed a distinction between (gradual) input to a process and output, which may be exponential. Unlike other approaches, the gradualism starting point is accepted here, establishing common ground for dialogue. It is, however, shown that exponential processes cannot produce nontrivial complexity gradually. Examples include building a tower of

blocks one at a time or a juggler gradually adding one pin. A biology case considered is bees' ability to solve the most researched problem in optimization, the traveling salesman problem (TSP). Starting from a working but inefficient algorithm, a TSP algorithm cannot be evolved gradually (by small step size, which, given evolutionary scenarios, must be much smaller than one line of code, approximately 16 bytes, allowing $(28)^{16} > 10^{38}$ possibilities)—not even by intelligent design! Arguing macroevolution in terms of parts (like irreducible structures) allows objections, linking it to microevolution, and algorithms make a better argument.

The “Pacemaker of the Ice Ages” Paper: Toppling an Iconic Argument for Milankovitch Climate Forcing

Jake Hebert

The authors of the 1976 “Pacemaker of the Ice Ages” paper computed power spectra using paleoclimatological data from two Indian Ocean deep-sea sediment cores. The resulting prominent spectral peaks corresponded to predicted Milankovitch orbital cycles and were largely responsible for today's widespread acceptance of the modern version of the Milankovitch theory. The paper, however, suffers from a number of serious problems. The most serious of these is that an assumed age of 700 ka for the Brunhes-Matuyama (B-M) magnetic reversal played a key role in assigning ages to two chronological anchor points in the longer core, but this 700 ka age is considerably less than the currently accepted age of 780 ka. This session is an update on research presented at the 2015 CRS meeting. Using data reconstructed from Figures 2 and 3 in the Pacemaker paper, I have successfully replicated the results from the paper's frequency domain analysis. I have also used the new age of 780 ka to assign new timescales to the two cores and to explore the effects that this change has on the results. Taking into account the new age for the B-M magnetic reversal dramatically weakens the Pacemaker paper. Because the modern version of the Milankovitch theory can be traced to this seminal paper, and because uniformitarians make extensive use of Milankovitch cycles to construct a secular geochronology, this is a potentially devastating result for uniformitarian dating schemes.

High Technology in Biology that Looks Like Ours

Daniel Currier

Many, like Behe, have noted the similarity of the structures and functions found in biology and our technology. Some

have called it “an echo of familiarity.” While many technological designs are inspired from biology, bioinspiration, many designs were created by human minds without knowledge of similar existing biological machines. Only later did we see their similarity. Biosimilarity, as I call it, describes the designs, shapes, and machines in biology that look a lot like our technology but arose independent from ours. While my goal is to eventually come up with a complete list of these, I would like to share a number of these biosimilar designs. Also, I want to make the argument that from universal experience, human minds are the only type of thing that can give rise to these types of structures, but humans were not the source for them since we contain some of these designs. Thus it follows that a similar but superior mind was the origin of these biological machines.

An In-Situ Lycopod Forest Site in Glasgow, Scotland, Invalidates the Floating Forest Hypothesis

Tim Clarey and Jeff Tomkins

The hypothesis of a pre-Flood floating forest ecosystem has its ideological roots in the nineteenth century. In the past few decades, this hypothesis has been promoted in the creationist literature as an explanation for extensive carboniferous coal beds. However, it was recently shown that this idea sharply conflicts with available geological data, timing of global coal deposits, and necessary hydrological factors to sustain a freshwater lens. In this paper, we present criteria for the recognition of true in-situ forests, within a Flood context. We have identified a site known as “Fossil Grove” in Victoria Park, Glasgow, Scotland, that meets nearly all the in-situ criteria. We propose that this site represents the remnants of a pre-Flood lycopod forest, with the fossil trees still rooted in a pre-Flood soil horizon, now lithified. Available oil well, outcrop, and seismic data support the conclusion that this site was not inundated and buried until midway through the rising portion of the Flood. Eleven fossil tree stumps were found to be spaced apart equidistantly with downward penetrating roots within a lithified clay-rich soil. We conclude this site represents an authentic, preserved in-situ lycopod biome. The fossil trees fit the same ecological schema as modern day lowland/swamp trees. In addition, we present evidence that conflicts with the speculation by some creationists that both the trunks and stigmarian roots of lycopods were hollow, a feature required to make the floating forest tenable. Based on this evidence, we recommend the floating forest hypothesis be abandoned.

The Paradox of Lazarus and Doppelganger Gene

Matthew Cserhati and Bendeguz Levente Szuk

The evolutionist François Jacob stated that two different species cannot follow the exact same evolutionary trajectory, since evolution is purely a blind process “tinkering away” with biological material. Genetically, this translates to the impossibility of the same gene randomly arising in a specific lineage two subsequent times.

Yet this is precisely what we observed in the distribution of so-called Lazarus and doppelganger genes (genes independently arising in the same or different lineages) shared, for example, between the starlet sea anemone, *Nematostella vectensis*, and a host of other organisms. One such gene, CaMKII is present in vertebrates, planarians, yeast, and thale cress. By using BLAST searches, we found between 302 and 2,117 homologous proteins between *Nematostella* (from JGI) and other major taxonomic categories (e.g., plants and mammals using the Uniprot protein data set). These genes are missing from bacteria and viruses, which precludes their having been horizontally transferred. We also found 7,779 ORFan genes in the *Nematostella* genome (28.5% of all genes) at an e-score cutoff of $1e-5$.

We also studied possible Lazarus genes present in bacteria and humans. Based on studies by other groups, we found Lazarus 119 genes which were not thought to be results of horizontal gene transfer. Distribution of bacteria genes in human is much less plausible due to the need to bypass multiple membrane systems as well as infect the germline.

We also found 2 Uniprot proteins that are present in vertebrates, fungi, plants, bacteria, and archaea, being thereby Lazarus and doppelganger genes simultaneously.

Can Iron Preserve Tissue for Millions of Years? An iDINO Progress Report

Kevin Anderson

The discovery of pliable tissue (containing cells and proteins) in dinosaur fossils has created a conflict between biochemistry and standard geologic dating paradigms. The assigned age of these fossils greatly eclipses known biomolecule decay rates. Various explanations have been offered for exceptionally long tissue preservation. The most popular is that iron from red blood cells will catalyze Fenton chemistry production of oxygen free radicals. Once produced, these free radicals will cause cross-linking of proteins, presumably making them more resistant to enzymatic and microbial degradation. In support of this model, a greater level of degradation was

reported to occur in blood vessels soaked in water compared to vessels soaked in iron-containing solutions. Yet, this study has many discrepancies, including failure to demonstrate that sufficient levels of iron can even be released from red blood cells. Ongoing work of the iDINO project has raised new questions regarding the evidence for iron preservation. Blood vessels were soaked in an assortment of solutions, which include water, glycerin, and hemoglobin. Microscopic observation found that some iron-free solutions provided a nearly equal level of preservation as iron-containing solutions. Also, red blood cells are not likely to be a sufficient source for iron, yet other natural sources also fail to provide adequate levels of soluble iron. This growing body of evidence challenges whether the iron model is a viable preservation system. Instead, a more consistent explanation is simply that the tissue has not been extensively preserved. Instead, the dinosaur fossils are only a few thousand years old.

Clash of Fossil Dating Systems

Hugh Miller

Results from radiocarbon (^{14}C) dating of fossils in the geologic column, including dinosaurs, fossil wood, and more, are at odds with conventional expectations by a factor of 2000. Volcanic products in strata coincident with nearby dinosaur bones have been assigned conventional ages ranging from 65 to 150 million years, often based on igneous bracketing of sedimentary strata using radioisotopes with long half-lives, for which a constant decay rate is assumed.

However, when one of the radioisotopes that is used for determining the age of the earth, ^{187}Re to ^{187}Os , with a half-life of 42 billion years, is in the plasma state (without electrons), the half-life speeds up a billion fold to 33 years. Since 99.99% of matter in the universe is in the plasma state, this constant becomes equivocal. Other phenomena are reported to speed up nuclear decay.

Our data show that ^{14}C dates for dinosaur bones and Pleistocene megafauna fall within the same range. Thus the assumed chronological gap between megafauna and dinosaurs does not exist, even if an unknown process influenced all ^{14}C results. ^{14}C dating of fossils also explains sequential strata in which megafauna and dinosaurs are found, and the absence of erosion between the strata. Sedimentological flume and field studies have challenged 19th and 20th Century theories on how sedimentary strata form. Pioneering research on ^{14}C dating of dinosaur bones, fossil wood, amber, coal, and diamond has been established, and it is now time to expand and publicize that effort.

Do “Varves” in a Japanese Lake Prove an Old Earth? Refuting an Argument by Old-Earth Geologists Gregg Davidson and Ken Wolgemuth

Jake Hebert

In the BIOLOGOS article “Christian Geologists on Noah’s Flood: Biblical and Scientific Shortcomings of Flood Geology,” the authors, Drs. Gregg Davidson and Ken Wolgemuth, present a number of arguments for an old earth. One such argument is that fifty thousand laminations (“varves”) in Lake Suigetsu (LS), Japan, prove that the earth is at least fifty thousand years old. Moreover, Davidson and Wolgemuth claim that good agreement between the varve counts and radiocarbon dates (as well as tree ring counts) prove that most of the LS laminations are indeed annual events. However, there are serious problems with the second claim, in particular. First, the “measured” amounts of radiocarbon within the tree rings were not measured amounts at all but rather were calculated from a northern hemisphere radiocarbon calibration curve. Second, Davidson and Wolgemuth failed to disclose that the yellow dots in their Figure 5 fell on their blue line only after the original varve counts were “corrected” by calibrated radiocarbon ages. Third, the LS varve chronology was a “floating” one: although the varve chronology extended to about 39 ka ago, the first varve age was assigned an age of 8.8 ka by finding the best match between the varve chronology and a composite tree ring chronology. Hence, the good agreement between radiocarbon “measurements” and the tree ring and varve counts actually results from a combination of circular reasoning and a failure on the part of Davidson and Wolgemuth to carefully read the original source material.

Continuous Environmental Tracking: Key Sensors and Condition-Consequence Processes

Randy Guliuzza

Are resilient creatures active trackers of environmental change by innate mechanisms enabling them to continuously fill new niches, or do geologic and climatic pressures predominantly drive adaptation in relatively passive organisms as in Gould’s lengthy account in *The Structure of Evolutionary Theory*? Or is it some combination of both? Principles of engineering may clarify operation of biological functions and offer some clues. Engineers always explain how designed entities work within the confines of its systems—especially mechanisms enabling dynamic entities to relate to variable external conditions. How do engineers obtain tracking capa-

bility? For an automated entity, they select distinctive tracking mechanisms to detect, and adjust to, specified deviations from norms in particular conditions. Core elements are sensors, condition-consequence logical algorithms, and response mechanisms. If tracking for interception is desired, then a chronometer is necessary. Creatures display the distinctive core characteristics. Sensors are the key element at entity-environment interfaces—the principle trigger of self-adjusting systems. Organisms’ sensors facilitate environmental tracking in four ways: (1) to detect and exploit specific properties of nature; (2) to detect external interface elements enabling mutual relationships; (3) to detect conditions specified to be a “stimulus”; and (4) for developing offspring to detect stimuli from parents. For the latter, molecular biology reveals networks of systems enabling great cross-generational physiological flexibility to environmental changes. Automation is demonstrated by irreducibly complex systems configured to function within a self-contained whole—without detected outside intervention.

An Event-Based Stratigraphic System for Describing Dynamic Flood Evidence

Nathan Mogk

Stratigraphy is a tool that is used to organize and communicate geological observations. A good classification scheme should organize data to naturally aid analysis. The biblical Flood is the most significant and transformative event to happen to the physical earth since its creation.

Given the dynamic and catastrophic nature of the Flood, extant stratigraphic methods, while useful in certain domains, are inadequate to establish relative timing of geological events over significant distances. Erosion and deposition of deposits that are sequential at one location may be synchronous or have the relative sequence reversed elsewhere, depending on how depocenters move in a dynamic Flood. This severely limits the range over which lithostratigraphic correlations can guarantee relative ordering of deposits, with uncertainty increasing with distance. Other stratigraphic systems have similar issues. With no categorization of relative timing appropriate to global flood conditions, it becomes difficult to analyze and communicate continental- to global-scale evidence clearly. This has bearing on several issues, including fossil ordering, the utility of radioisotopes as a relative age indicator, and the appropriate use of the Uniformitarian Chronostratigraphic Column.

I propose an event-based stratigraphic system that is designed to deal with a complex network of interacting causes over a large range of extents, including global. In addition to events, actions by agents are also considered, which allows

the connection of geological evidences to God's purposes and direct actions. Once a full sequence of events is identified, then absolute timing constraints on individual events can be estimated from the time available.

Are Birds Dinosaurs?

Matthew Speights

The prevailing scientific paradigm today for the origin of birds is that birds evolved from small theropod dinosaurs. Evolutionists point to similarities between birds and theropod dinosaurs and claim that they are homologous, evidence of common ancestry. A much smaller group of evolutionists has claimed that birds evolved from another group of reptiles besides dinosaurs. The typical creationist response has been to claim dissimilarity between birds and their alleged dinosaur ancestors or to question the interpretation or authenticity of fossil evidences for bird-dinosaur similarity.

A different model from either the primary evolutionist or creationist explanations is proposed; namely, that birds can be considered dinosaurs even in a creationist framework. The historical creationist reaction against the concept of birds as dinosaurs has been driven primarily by a misunderstanding and conflation of terminology and ideas. The semantic aspects of the debate will be explored through the history of taxonomy, including classification frameworks such as folk and functional taxonomies, as well as Linnean, phenetic, and cladistic methods. Also addressed will be common objections raised by creationists against purported similarities between birds and theropod dinosaurs. Birds are morphologically similar to one group of dinosaurs, a similarity that will be explored by examining the anatomy of fossil and extant species. In a biblical creationist worldview, the phrase, "birds are dinosaurs" can be used in a way that is both accurate and meaningful, while still rejecting evolution.

The Apparent Age of the Time-dilated Universe: The Magnetic Orbital Decay of Close Solar Type Binaries II

Ron Samec

In creation time-dilation cosmologies, one major question is, "What maximum apparent age should be used to characterize the universe?" In this presentation, one particular age indicator is used. My larger plan is to determine estimates of the answer to this question for many age-bearing processes and then to give a reasonable answer to this question. In this case, I am pursuing geochronology, the precise derivation of

stellar ages from the orbital periods of single stars and interacting binaries. Here, I correct the earlier study, and I expand the results paper using a simpler algorithm that applies to many more binaries. I increase the number of binaries in the earlier study from 18 to 124. The only basis for the selection of these systems is that they appear to be undergoing a clear and preferably long, decaying orbit indicative of magnetic braking. This is shown by a negative quadratic term in dP/dt (days/year), where P (days) is the orbital period of the binary. As before, I attempt an age estimate of these solar-type binaries apart from evolutionary time constraints assuming an initial period at the creation (or formation) of the binary (here, 5–20 days).

Synthesis of Genetics and Linguistics Uncovers a Potential Third Explanation for the Map of Human Origins Derived from Both Fields

Nathaniel Jeanson and Les Bruce

Recently published findings suggest that mitochondrial DNA (mtDNA) might be a useful tool by which to confirm the biblical record of human origins. The number, structure, and relative patterns of human mtDNA differences seem to echo the existence of a single female progenitor of the human race (Eve), the population bottleneck at the Flood, and the population dispersal following the Tower of Babel episode. This concordance suggests that mtDNA might also be a useful tool by which to interrogate additional aspects of human origins on which Scripture is silent. However, in terms of cause and effect, the primary earthly mechanism by which God separated the people groups at Babel was linguistic, not genetic. Since this linguistic cause would certainly have secondary genetic effects, we were curious to know if genetics and linguistics could synergistically inform one another and flesh out a fuller picture of human origins. We created separate geographic maps of humanity based on genetics and linguistics and then examined whether the datasets agreed. The mappings indicated several points of correlation, whereas other areas did not appear to correlate. Conversely, we found that both maps seemed to be overlaid with a third factor—migrations recorded in extrabiblical human history. If conquests and economically motivated population mixing within recorded human history are sufficient to explain human genetic origins and current linguistic relationships and distributions, this would present a strong challenge to the evolutionary model and further underscore the veracity of the human history record in the Scriptures.

The Fallacious Nature of All Old-Earth Arguments

Jason Lisle

We examine the logical structure of the scientific arguments used to support the idea that the earth is billions of years old in contrast to the history given in Scripture. We find that all the commonly used arguments are not cogent when examined from a worldview perspective because they all commit the *petitio principii* fallacy. Such arguments tacitly and arbitrarily presuppose conditions that are reasonable to hold only if biblical history is rejected. Hence to use such age estimates as an argument against the biblical timescale is fallacious, since it begs the question. Conversely, young-earth arguments are generally of the *reductio ad absurdum* variety and are logically cogent. Creationists who understand these principles will be able to refute any old-earth argument.

Continuous Environmental Tracking: An Engineered Method to Fill the Earth

Randy Guliuzza

Increasing evidence shows that God engineered creatures with systems to detect changes in myriads of external conditions and then effect change—suitable self-adjustments that actively sustain a close and continuous tracking of environments. The inferred purpose is to fill niches. In addition, studies demonstrate that parental self-adjustments via heritable epigenetic chromatin modifications and other transmissible non-chromosomal factors (including heritable RNAs) are utilized by offspring. During development, descendants express even tighter change-suitable modifications. Thus, whole populations with self-adjusting capacity preceding environmental change may ratchet closer tracking of variable conditions through spatial gradients and time dimensions. Two implications follow. First, continuous environmental tracking is a way that God reveals His creature's extraordinary self-adjusting ability. What emerges is not a static picture but mechanisms promulgating a spectacular kaleidoscope of innovative solutions to environmental challenges—demonstrating the depth and breadth of God's engineering genius. Second, robust organisms regarded as resilient, active trackers contradict the standard evolutionary view. Medina's 2010 paper, "Natural Selection and Self-Organization: A Deep Dichotomy in the Study of Organic Form," details that most evolutionists see organisms as "passive," driven by mindless vicissitudes of environmental challenges over time, and that their changing forms are "imposed [on them] from without." This follows how Darwin "accepted the view that the environment directly instructs the organism how to vary ... the

organism was like modeling clay" (Kirschner and Gerhart 2005) shaped by its environment making them only appear as designed.

The Gezer Connection: Solomon, His Pharaoh Father-in-Law, Shishak, and Hatshepsut

Anne Habermehl

This paper will show that Solomon's father-in-law was most likely Thutmose III, who captured and burned Gezer and presented it to his daughter, Solomon's bride, as a wedding present. Examination of the geography of Canaan shows that the cities that Thutmose III captured in his campaigns are located along the Mediterranean coast but are not within the territory of Solomon's kingdom. Hatshepsut was aunt/stepmother to Thutmose III, and the end of her reign possibly overlapped with the beginning of Solomon's reign for a few years (although she was not the Queen of Sheba). Shishak was most likely Amenhotep II (son of Thutmose III), who was friendly with Jeroboam, first king of Israel in the divided kingdom. A difference of about 470 years between the biblical and secular timelines at the time of Solomon is therefore postulated. This figure is independently calculated and supported by placing the Exodus at the end of the reign of Twelfth-Dynasty Amenemhat IV, and revising Dynasties 13 and 14. Drastic shortening of the Egyptian timeline from the Nineteenth Dynasty on will be required to make it correspond to the biblical timeline. Correlation of these two divergent timelines is important because unbelievers use their secular timeline to claim that the Bible is inaccurate in its historical statements.

Abiogenetic Disconnects: How Entropy Works Against a Natural Origin of Life

Timothy Stout

Entropy dooms abiogenesis. *Abiogenetic disconnects* explains how. Since a functioning, living cell is far too complex to make a sudden, single-step appearance, abiogenists propose that living cells eventually emerged by natural processes working through a series of steps to produce ever-increasing degrees of organization.

In general, multiple hundreds of thousands of different chemicals can be formed from carbon, nitrogen, and miscellaneous elements. Each proposed step of abiogenesis can turn its starting products into a broad distribution of potential output products. There will be a natural ratio of products produced from the many that are possible to be formed by the natural process(es) working on them. By

contrast, abiogenesis is very specific in its requirements. Only a small portion of any one step's products will be suitable for an advance in abiogenesis. The problem is that there is no connection between the principles determining which of the broad-ranging scope of products are produced at any given step versus which products abiogenesis needs at that step. The natural ratio doesn't provide the species required for abiogenesis in the required ratios, in the required purity, and at the required locations. There is nothing to constrain the broad-ranging products naturally produced at any step to be those required for abiogenesis. Entropy guarantees that the broad products will dominate a step, not those abiogenesis needs. A simple perspective thus reveals how entropy renders abiogenesis impossible. This impacts every step of abiogenesis.

Geology of Wisconsin and the Upper Peninsula of Michigan

Stacy Lung

Significant work has been done in developing a geologic timeline that supports the biblical creation. This paper utilizes current geologic research and understanding to explain the landscape features of Wisconsin and the Upper Peninsula of Michigan. Locations were selected to provide a chronological "tour" of the geologic processes that operated during the stages of the global Flood and subsequent Ice Age.

This paper first considers sites with geologic characteristics of the Flood onset, including the midcontinental rift system. Locations with evidence of widespread, regional sedimentary deposition and sedimentary features, like cross-bedding and fossil beds, are used to illustrate middle-of-the-Flood processes, when the waters covered the land surface. The receding Floodwaters are seen in the geology of the Mississippi River area and in the formation of karst features. This is ultimately followed by glacial evidence from the

post-Flood Ice Age in the geologic chronology presented.

As the evidence for a biblical, geologic timescale continues to grow and improve, it is necessary to apply this framework to additional locations and situations. It is also important to make this information accessible and to provide alternatives to the old-earth explanations offered by most guidebooks and park system resources. Input into the interpretations and applications within this paper could help provide this alternative for the unique geology of the Wisconsin area of the Lake Superior region.

How to Write a Scientific Abstract: Do's, Don'ts, and Nevers

Kevin Anderson and Robert Hill

An abstract is a short summary of completed research. The purpose of an abstract is to help the reader decide whether to read the entire article or go to the conference presentation. Abstracts should explain the justification for conducting the research, the methods and procedures employed, the results obtained, and the conclusions and implications of these results. This talk is intended to help prepare attendees to write quality abstracts about their own research. Organizational structure and basic guidelines of a scientific abstract will be discussed as well as common mistakes to avoid.

Effective PowerPoint Presentations

Robert Hill and Kevin Anderson

PowerPoint is a powerful tool for giving presentations to groups of people. Unfortunately, it can also be used as a crutch for a bad presentation. This talk will help prepare the attendees to develop better PowerPoint presentations for their own talks. Properties of good presentations will be discussed, as well as common mistakes to be avoided.

Letters to the Editor

The policy of the editorial staff of CRSQ is to allow letters to the editor to express a variety of views. As such, the content of all letters is solely the opinion of the author, and does not necessarily reflect the opinion of the CRSQ editorial staff or the Creation Research Society.

Mis-understanding Genesis 1

The exchange of letters “A Young and Old Earth,” between David P. Nelson and Danny R. Faulkner in the Winter 2016 CRSQ points up how much quibbling over days in Genesis could be eliminated by application of good writing principles taught us in grade school. Our teachers pounded into our heads that every presentation should have an introduction, body, and conclusion. Moreover, each paragraph should deal with just one idea, or one aspect of an idea, using a connecting word or phrase to tie it to the previous paragraph, then explaining the aspect or idea and concluding with a summary or lead-in to the next paragraph.

Most every article in CRSQ follows this type of format. Even Nelson does this in his letter. If this has been so long a measure of good writing, should we not also expect to find similar formats used in Scripture, given that the English Bible was so long the only text used in schools to teach reading and writing? In our society, principles of good exposition were derived from inspired Scripture.

Genesis 1:1 and 2:1 form a solid literary unit called an *inclusio*. When the form of an *inclusio* is recognized, it will have beginning and ending summary statements that say essentially the same thing. Everything in between those summary statements will be about one topic only. “*In the beginning God created the heaven and the earth. ... Thus the heavens and the earth were finished, and all the host of them.*” The two verses are parallel ideas. Everything in between these two verses is what happened *in the beginning*.

Since Genesis 1:1 is a summary statement and the beginning is the time of the events described in 1:2 through 1:31, Genesis 1:1 can have nothing to do with an imaginary period prior to 1:2, for there was no temporal existence prior to *the beginning*. Note 1:2 says, “*And the earth was ...*,” a brute fact of being created and made extant, an event of coming into existence by the will of God, not that it took millions of years to agglomerate, or heat up, or cool down. There is no difference if one thinks *earth* in this context might mean the planet we’re living on, or, more generally, matter, or electric charge, or water molecules, or plasma.

During a 2006 2-day seminar at the Logos Building in Orange County, California, Dr. Glen Collins made the point that the events in Genesis 1 are *events*, of the nature that “God spoke, and it was so.” Genesis 1 is not a description of process; especially not processes that would take a long time. Nor does it tell us how God made things, as though we could duplicate His work out of eternity. Rather than millions of years of “prehistory,” so-called, the real takeaway from Genesis 1:1 is later stated in Scripture: that the things which are seen were made from things which are invisible (Hebrews 11:3). Put in philosophical jargon: that which is temporal is contingent upon that which is eternal.

Ancient peoples thought of time, not as a linear progression along an arithmetic sequence of defined intervals, but in relation to events. There was no concept of “progress”; so order of events on a time line was unimportant. Only the “quality” of the time was important, which was

determined by the events that occurred and their effect on the quality of life of the people of the time. Sequential ordering along a timeline was more a memory aid to those who would learn and retell the story. (A similar principle applied to the concept of “weight” in ancient Egypt. Gold was poured into a standard container and then put on a balance against standard weights. The idea was not that it “weighed” so many standard units but that a standard volume of it was of better *quality* if it tipped the balance. They even applied this idea of testing the quality to the weighing of the heart ritual in the afterlife.)

That Genesis 1 is historical narrative was well demonstrated in the RATE project by statistical comparison of Hebrew verb forms in the different genres of Scripture. What also needs to be considered is the *purpose* for which God inspired Moses to set it down in writing. That is revealed later in Scripture, when God said He would make of the Israelite slaves in Egypt a new nation ... a great nation ... having the oracles of God ... a light to the Gentiles. Every nation needs a basic mythos, explaining their origin, cultural and religious principles for living life, and sense of purpose and ultimate destiny. Coming out of generations of immersion in pagan, Egyptian culture, the people who would become the new nation of Israel immediately needed to know who God is, what He is like, and how to worship Him. God gave them the Law of Moses.

The reason Genesis 1 recapitulates specific events of Creation is that those events directly oppose the pagan creation myths of Egypt (and other pagan reli-

gions) in detail. Likewise, the 10 plagues of Egypt showed God's power over all the elements of nature and the pantheon of Egypt's supposed "gods." Ancients had the concept of the *Order of Creation*. Genesis, inspired by the one true God, the only true witness to the events, gives the true Order of Creation. *Order*, in this context, is about superiority, priority, and power much more than any details like laws of physics, timelines, or what we might conjecture about origins and cosmology from the brief statements in Genesis. All those other things with which we concern ourselves are greatly diminished in light of God's superiority,

priority, and power! (Compare Hebrews, which is all about the superiority of Jesus Christ to all things in heaven and earth.)

Oh, you demand a conclusion? There are only a few hints in Genesis 1 and 2 about things God might have taken more than an instant to do; e.g., gathering the waters together unto one place. Or one could imagine the grass growing up, not instantly, but in a day, like the gourd God made for Jonah. The author has imagined that God could very well have created the entire creation, fully ready to function, in his eternal realm, and simply dropped it into temporality and activated it in an instant.

Such an unveiling of the Greatest Artist's and Greatest Engineer's work would conform nicely to God's character and power. But if God formed Adam from the dust of the ground and breathed life into him, it seems to mean He did at least one act of creation using starting material He had already created. And that seems to militate against the author's idea! The only reason the author can see for God to take 6 days plus a day of rest is moral, as the type for the workweek and day of worship.

George P. Drake
Santa Ana, CA

A Young-Earth Creation Model for Genesis 1:1–19

I am writing this in response to the letter by David P. Nelson (Nelson, 2016) and the editor's response (Faulkner, 2016) published in the recent *Creation Research Society Quarterly*. As pointed out by the editor, the letter by Nelson proposed an interpretation of these verses of Genesis that allowed a separate chronology for the heavens and the Earth with a gap between. I have proposed a more physically coherent interpretation and model for this same text (Dobberpuhl, 2011a) that closes the gap into a single chronology for both. The following synopsis points out the differences in our interpretations, retaining Nelson's order of presentation.

In the Beginning

The main difference in our interpretations begins with Genesis 1:1–2. He

interprets that these verses pertain to God creating a planet Earth on the first day. When God is the subject of the verb *bara*, it should be interpreted as making something from nothing that preexisted (Hebrews 11:3). From Genesis 1:10, the Hebrew word for earth should be interpreted as the material that makes up our planet. Dry ground is a combination of all the chemical elements found in the universe. Everything in the physical universe also contains most of these same chemical elements, even seawater.

According to verse 2, the original created earth material was unformed and a liquid that did not emit electromagnetic radiation (EMR) or light. A planet has the form of a sphere. It also emits EMR or light (Dobberpuhl, 2011b). It could not be totally made of molecular water or any other material made of atomic

matter. The Hebrew word for waters used in Genesis 1:2–8 should be interpreted as describing the as-yet unknown universal liquid material (earth). It is used as a substitute for the earth material as the material is transformed from one liquid to the next. One reason for using this substitution in these verses would be that there is no other Hebrew biblical word for a generic liquid.

Asah, Natan

I am surprised that the Hebrew word for create (*bara*) was not included in this paragraph. It is the key to the interpretation of the two words that Nelson addressed. The word for create is used only this once, in verse 1, of the 19 verses under consideration. Because of this fact, a good definition of both *asah* and *natan* should always include the created

material earth that God transformed or made into something new or different with each miracle. I agree with Nelson's definitions of these two words but only as God doing something to an already created material, as described in the verses that precede the verses of their use. This interpretation fits everything that God did with the miracles He performed into a single chronology for the heavens and the planet Earth.

Days One, Two, and Three

At this point Nelson's interpretation and model becomes incoherent. God commanded light to come into existence in verse 3 so that light or EMR did not exist prior to that miracle. The liquid material could not have been atomic matter since atoms or their subatomic particles are continuously emitting EMR. What God did by bringing light into existence at dawn of the first day was to form both light (Isaiah 45:7) and its source atoms from the created earth material. With this interpretation the original physical heavens of the first day was a three-dimensional volume that contained only the single blob of liquid earth material. There was no planet Earth covered by water and clouds rotating in an unidentified light source from a single direction to produce the night and daytime of the first day. Why would God shield visible light from eyes that did not exist on the first day?

On the second day, God made the expanse that He named heavens according to verses 6–8. He did this by dividing up the single blob of liquid material that He had at least partly transformed into atomic matter and EMR. The division was not into two parts but into billions of galaxy seeds. He separated these galaxy seeds from each other with space, causing relative darkness for the first half of the second day. These galaxy seeds ended up positioned throughout the physical universe. At dawn of the second day, each galaxy seed expelled the atomic material that formed into

the celestial bodies of that galaxy. The atomic material was still in fluid form and emitted EMR to provide the light for the second daytime. One of those celestial bodies was the primordial planet Earth, and the remainder formed the large-scale structure of the expanse, or stretched-out heavens.

By the beginning of the third day, the Earth had cooled enough that pockets of molecular water and gases could form under its surface. These pockets of molecular water and gases burst through the surface to first cover the whole surface with water and generate an atmosphere (Job 38:8–9). In Genesis 1:9 God commanded the waters to gather into seas while what became dry land rose above sea level to enclose them (Job 38:10–11). God next caused the seeds of all the kinds of vegetation to form within the dry land. These seeds sprouted and grew into mature plants within less than one day to bear seeds that continue to propagate their kind.

The Fourth Day

A translator or interpreter is not allowed to rewrite the original text as Nelson has proposed for verses 14 through 17. His model requires that the celestial bodies were created before the first day. He does not understand that when God says, "Let there be lights in the expanse of the heavens" that the expanse did not exist until the second day and that there were no stars providing light before that moment on the fourth day. The celestial bodies that became stars on that day were made on the second day, or God would not have named the expanse heavens. They remained dark on the third day (Job 9:7) and lit up on God's command at the beginning of the fourth day. This included the sun that provided light for the moon, Earth, and all the other planets in the solar system. The other stars and their stellar systems were in their relative positions in the sky so that they provided the signs for seasons, days, and years as constellations.

The light-travel time problem Nelson attempts to avoid has a better solution in that God has the ability to speed up or slow down the light traveling from the stars. Even the stars visible to the human eye can be up to 6,000 light-years' distance. For the constellations in the sky to be visible on the fourth day, light would have traveled that distance in 24 hours or less. For God that is not impossible.

Light

It is another surprise that Nelson left this paragraph until after his discussion of the fourth day. God formed light on the first day according to Genesis 1:3–5. I assume He formed it from the earth material because that was the only material available. I agree that it involved the entire EMR spectrum and the remainder of what he discusses about the characteristics of light. I strongly disagree that light had to exist prior to verse 1. A better interpretation of the text is that light (EMR) was freed from the original earth material to make atoms that are the source and absorbers of light even today.

Problems Resolved and Remaining

Nelson's assumption that a planet Earth was created at the beginning causes more problems than it resolves. Isaiah 45:18 says God did not just create the earth but formed, made, and established it. Several other references state that God laid the foundations of the planet, including Psalm 104:5. What reason was there for God to take these actions if He could have created the planet in its final form? The same could be said about the heavens. Genesis 1:6–8 says God made the heavens, and Isaiah 42:5 (plus many other references) says God stretched them out. I interpret the stretching out of the heavens as the separation and dispersal of the liquid earth material that involved the stretching of the gravitational fields between them. Isaiah 40:26 says God led out the stars one by

one. What reason would God have to make and stretch out the heavens and then lead out the stars if He had created them all before verse 1?

In this paragraph there is another example of Nelson attempting to change the biblical text to match his interpretation and model. The Exodus 20:11 and 31:17 references support a better understanding of the Genesis 1 account of Creation, and they surely do not need revision. All that is required is for Nelson to change his understanding of the

original heavens and earth. They were a three-dimensional space containing only a single blob of a mysterious earth material that was used by God to make the heavens and earth that existed after the fourth day. There is no need to change any biblical text to fit this interpretation and model. For more details and speculation based on this model, see Dobberpuhl (2011a).

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The Modern Creationist Movement—Repeating History?

North America in the early 1900s saw the birth and rise of Fundamentalism, a movement driven by the need to affirm biblical orthodoxy and defend it apologetically against the encroachment of liberal theology, German higher criticism, and a host of other sub-biblical ideologies. With the publication of *The Fundamentals* (originally printed between 1910 and 1915), the movement's defense of orthodoxy was crystalized around five points: the inerrancy of Scripture, the Virgin Birth of Christ, the substitutionary atonement of Christ, the bodily resurrection of Christ, and the historicity of the miracles recorded in Scripture. Only at the risk of coming across as singularly foolish could a genuine Christian question the nobleness of this objective.

However, as the decades progressed, Fundamentalism became deterred from

its noble goal. The defense of biblical orthodoxy commonly took a back seat to advocacy for "reform" in areas more commonly regarded as matters of Christian liberty. Fundamentalism came to be characterized more by its opposition to drinking, movies, and card playing than its quest for purity in doctrine. Near obsessive focus on "separation" stifled the virtues of the movement, relegating it to cultural irrelevancy and often giving the impression (warranted or not) of anti-intellectualism. Although some individual fundamentalists were intensely focused on the central theological aspects of the movement and did make remarkable contributions, they were the exceptions.

What is genuinely disconcerting about the brief history of Fundamentalism is that the modern creationist movement appears—at least from my

vantage point—to be following in exactly the same pattern. Many biblical creationists, while acknowledging the earlier roots of the movement, look to the publication of *The Genesis Flood* in 1961 as effectively marking the beginning of *modern biblical creationism*. The movement's initial objective was markedly evident, clearly implied even when not definitively stated. In short, the modern creationist movement centers on the defense of the biblical record of creation as God-breathed truth. It maintains the biblical text gives an elementary yet scientifically accurate description of God's creative actions. The biblical record, furthermore, is of foundational theological importance and resists efforts to accommodate it to man's conjectural notions concerning cosmic and/or biological evolution. At its core, the creationist movement seeks

to uphold the ultimate *authority* of the Scriptures.

Nevertheless, this objective, once so very much the lifeblood of the creationist movement, is all too often sidelined by other less edifying and less productive concerns. Like the Fundamentalist movement, which allowed secondary or tertiary doctrinal matters to detract from the defense of the fundamentals themselves, so I fear the creationist movement has allowed matters of obscurity to overshadow the real work of upholding biblical authority—and in so doing has undermined a stable foundation for bearing forth the gospel witness. Why, if the defense of biblical authority is of supreme importance, has so much ink been spilt by young-earth creationists on peripheral issues such as the exact landing site of Noah's ark, the degree to which the Tower of Babel was completed before God's judgment, the meaning of Methuselah's name, whether God required a blood sacrifice of Cain, or even the existence of the mysterious *mokele-mbembe*?

It is not that these subjects are not interesting in their own right; however, the increasing trend has been to focus on these nominal curiosities, rather than on building robust models to enhance our defense of biblical authority in those critical areas where it is being attacked—the age of the earth, the historicity of Adam, and the goodness of the original creation. Not only has increased attention been given to these peripherals, some creationists have grown inexplicably dogmatic in the defense of their views on such matters. For some creationists,

each individual detail of their outlook on the interpretation of Genesis 1–11 is held with equally unwavering tenacity, almost as if their whole apologetic case for biblical creation hinges *on that one point*. Even more alarming, some of the positions so dogmatically held by creationists are flatly contrary to what the Bible actually says. In the interest of brevity I will cite only one—startling—example:

In browsing through my file cabinet where I keep printouts of noteworthy articles on biblical creation, I came across no fewer than half a dozen articles published in the last ten years which claim explicitly (allegedly on the basis of Genesis 3) that the Lord *cursed* Adam, Eve, and the process of childbirth. This assertion is both unnerving and unbiblical. On an exegetical level, we must ask the question, *Where in the biblical text does it say that man, woman, and childbearing were cursed?* Nowhere. In fact, in Genesis 3, the Lord expressly curses only the Serpent and, on account of man's sin, the ground. While Adam and Eve reap deadly consequences for their own sin, never does the text say that they (or childbearing) are cursed. Thus, at the very least, to propose that mankind and childbearing are cursed is sloppy exegesis. On a theological level, however, there are even graver concerns. Could Jesus Christ, the perfect, unblemished, *yet fully human* sacrifice given for the sins of the world, have come (with respect to His human origins) from a cursed heritage and entered into creation by means of a cursed mechanism?

Plainly, the theological ramifications of such a notion strike at the very core of orthodox Christology. And yet this is what the articles in my file were claiming as if it were unquestionable fact.

If the modern creationist movement is to succeed in keeping itself from retracing the steps of Fundamentalism, there must be a return to the central objective of upholding biblical authority, and of necessity, therefore, of giving utmost attention to rightly understanding and defending *what the Scriptures actually teach*. We must resist the inclination to retreat, as Fundamentalism did, into a morass of infighting; and we must avoid the inclination to dogmatically contend for our perspectives on peripheral issues as if they were the chief matters of Christian orthodoxy. Only in conscientiously doing these things can we correct the present trajectory of the creationist movement and keep ourselves from the peril of repeating Fundamentalism's failings.

This is indeed a challenge, but, thankfully, we are not without the Lord's gracious aid. We as biblical creationists *can* move beyond our current predicament if we commit ourselves to learn from the patterns of history, attend to the truth of the scriptural text (rightly interpreted), and give heed once again to creationism's noble objective of upholding biblical authority.

Will we do this? I pray that indeed we will.

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Media Reviews



Dinosaur Blood and the Age of the Earth

by Fazale Rana

RTB Press, Covina, CA, 2016,
116 pages, \$14.95

The discovery of tissue and protein fragments remaining in dinosaur fossils poses a direct biochemical challenge to the standard geologic dating paradigm. If dinosaur fossils are at least 65 million years old, how has this biological material survived? How could these bones not yet be fully fossilized even after millions of years? These are not irrelevant questions asked only by creationists. Many evolutionists understand the obviousness of these questions and the issues such questions raise about their dating system (Anderson, 2016).

The Creation Research Society's iDINO project has been actively studying dinosaur tissue as well as investigating mechanisms of how this tissue is supposed to have been extensively preserved. The 2015 special iDINO report in the *Creation Research Society Quarterly* (vol. 51, no. 4) has summarized some of the iDINO work. Because this special issue of CRSQ is so prominently featured in Fazale Rana's *Dinosaur Blood*, it is tempting to speculate that the iDINO project, and specifically this issue of CRSQ, prompted Dr. Rana to write this book.

Rana is a chemist for the Reasons to the Believe ministry. As such, he supports the standard geologic dating scheme that places dinosaurs over 65 million years ago in earth history. Understanding the dilemma presented by the tissue, Rana wrote *Dinosaur Blood* to justify why this tissue cannot be used to date these fossils or as evidence that these fossils are dramatically younger.

He acknowledges that after the discovery was publicized, many scientists had serious doubts about the authenticity of the tissue. He provides a brief discussion about claims that the tissue was actually bacterial biofilm, modern bird, or other forms of contamination (pp. 25–26). He even quotes a journal reviewer who said this type of preservation is not possible, regardless of what the data show (p. 26).

Recognizing that the evidence now clearly demonstrates the extracted material is actual dinosaur tissue (p. 26), Rana seems to assume that everyone else now recognizes its authenticity too. Thus, he apparently believes this period of denial is long over. He even declares that “soft tissue discoveries trouble virtually no scientists” (p. 12), indicating the tissue poses no problems for geology or paleontology.

However, in saying this, he ignores the continuation of denial and dismissal. Claims are still made that the extracted material is contamination, lab error,

biofilms—anything except actual dinosaur tissue. For example, writing for Smithsonian.com as recently as 2012, Brian Switek (2012) still tries to suggest the tissue “may be microfossils created by bacterial biofilms,” and even leaves dinosaur tissue off of his 2014 list of unsolved dinosaur mysteries (Switek, 2014). In an evaluation of creationist articles, Nieminen et al. (2015) chastise creationists for discussing dinosaur soft tissue because they claim the discovery has been refuted. Also, as of 2015, the Carnegie Museum of Natural History (Pittsburgh) still claimed there are “no original organic parts preserved” in fossils (Thomas, 2015, p. 239).

In addition, I have observed that there is an overall lack of discussion about the tissue discovery within the scientific community, even within contemporary geology and paleontology curriculums. Considering the significance of the find, this seems rather odd. I have communicated with graduate students in biology and paleontology who have no knowledge of the tissue discovery or are still being told it is just contamination. This is not consistent with Rana's claim that “soft tissue discoveries trouble virtually no scientists.” This seems more consistent with attempts to ignore the topic altogether rather than efforts to explain it.

In truth, the tissue discovery has, and continues to be, greatly troubling

to many within the evolutionary community (Anderson, 2016). Rana's intentional downplaying of these dismissals gives warning to his highly selective eschewing of the history and ramifications of this discovery. It also serves as a possible warning to the reader of his selective approach to evaluating data.

The basic arguments Dr. Rana offers in *Dinosaur Blood* fit into two general categories: (1) age of the earth and (2) chemistry of the tissue.

Age of the Earth

Rana devotes a significant portion of *Dinosaur Blood* to describing why he thinks the evidence for a multibillion-year-old earth is solid and indisputable. He adamantly assures the reader that radiometric clocks are valid (pp. 37–51) and that an “old earth” position is not only biblically viable but even superior to a “young earth” position (pp. 77–81). From this he concludes that the presence of tissue and proteins, while interesting, does not warrant dismissing the secure and accurate dates already assigned to the dinosaur fossils.

His discussion of radiometric dating draws upon fairly standard arguments for the accuracy of the technique. He points to its wide acceptance in the scientific community, even by scientists who are Christians (such as himself). He also suggests the technique has been verified by numerous independent tests and has withstood the test of time (pun slightly intended).

He finds great comfort in G. Brent Dalrymple's writings about radiometric dating (p. 39). Rana views Dalrymple as objective and trustworthy, even observing, “I have no reason to think he harbors any animosity toward Christianity” and “has no ulterior motive when he makes the scientific case for the antiquity of the earth” (p. 39).

Regrettably, such conclusions involve faulty reasoning, if not abject naivety. As an ardent evolutionist, Dalrymple has an unwavering commit-

ment to the evolutionary timescale and its presumed multibillion-year history. A lack of animosity toward Christianity is irrelevant. Unless he is ready to fully abandon his evolutionist philosophy, Dalrymple has no alternative. His “motive” is to defend the evolutionary timescale from all criticism regardless of the data.

A few specifics are also worth noting. Radiometric clocks assume that (a) radiometric decay has always been constant, (b) amounts of isotope in the sample are not affected by external processes, and (c) a newly formed rock would contain only trace amounts of daughter isotopes (those elements resulting from radioactive decay). Each of these involves major assumptions, often unacknowledged by the general scientific community. Each of these assumptions also has been strongly challenged (Vardiman et al., 2005; Snelling, 2009). In particular, evidence indicates that significant amounts of isotopes can frequently move in or out of a sample over time. Rana offers some brief rebuttals but ultimately fails to seriously answer these challenges.

For example, Austin (1996) obtained a 350,000-year potassium-argon (K-Ar) date from recently erupted Mt. St. Helens lava rock. Rana simply dismisses this as a demonstration that K-Ar cannot be used to date recently formed rock (p. 43). He argues that this incorrect date was because “young” lava rock sometimes contains parentless argon (i.e., argon that did not originate from the slow decay of potassium after the rock was formed, which is actually a violation of assumption c above). Rana concludes that this parentless argon caused the erroneously high K-Ar date reported by Austin (1996). However, he does not explain how geologists are supposed to determine whether the argon is parentless or not. There is no distinguishing chemical test.

Rana also proceeds to undercut his own assertion about parentless argon.

He cites Kenneth Miller's claim that rocks in an earth formed just a few thousand years ago “would contain little or no argon” (p. 47). Why? Could not rocks from this “young” earth also contain parentless argon—the same parentless argon that he just invoked to explain the erroneous K-Ar date of new lava rock?

Thus, Rana follows a practice all too frequently employed to explain discordant radiometric results that threaten a belief in a multibillion-year-old-earth. His “old earth” position forces him to accept the existence of “parentless” argon for some rocks but not for other rocks. The only determining factor is whether it fits his belief system. He claims parentless argon is present when it supports his position but then ignores the possibility when it does not. In so doing, he fails to acknowledge that if parentless argon can exist in some lava rocks, then it can certainly exist in any lava rock.

In fact, there are numerous examples of excess argon in rock known to be “young” (Snelling, 2000). This indicates parentless argon may be fairly common. Could there also be high levels of parentless argon in most contemporary lava rock? This would easily make all these rocks “appear” much older than their actual age? Just the possibility raises numerous issues with Rana's attempted explanation, rendering it virtually meaningless.

In addition, Rana addresses Thomas and Nelson's (2015) report of carbon-14 (C-14) in dinosaur fossils. Because of the 5,700-year half-life of C-14, fossils older than 100,000 years should no longer contain detectable levels of C-14 (i.e., carbon dead). Since dinosaur fossils are considered far older than 100,000 years, the presence of C-14 creates a paradox. Rana suggests this C-14 has come from extraneous sources; most likely (a) C-14 from contaminating microbes and other contemporary organic material, (b) contamination from a background of atmospheric C-14, and (c) exposure to

uranium and thorium, causing a conversion of nitrogen-14 to C-14 within the fossil (pp. 49–51).

These are all potential contributors to C-14 levels in fossils, but Rana fails to successfully demonstrate that they are more than minor factors. Contamination, whether from a microbial or environmental background, would almost certainly reveal itself with inconsistent and widely fluctuating levels of C-14 in various fossils. Such wide fluctuations are not found regardless of the specimen's size, type, or geologic location (Baumgardner, 2005; Thomas and Nelson, 2015). In addition, preparation of samples for C-14 analysis is very rigorous, minimizing any contamination from handling the samples (Snelling, 2008). Also, Rana fails to do the math since highly unrealistic amounts of uranium and thorium are necessary to account for any significant level of C-14 in dinosaur fossils (Russell, 2004).

Rana also states that if the dinosaur fossils were actually only a few thousand years old, they should have much higher levels of C-14 remaining. Thus, he reasons that the small amounts of C-14 still detected in these fossils are strong proof of contamination (p. 50). However, this assumes the level of atmospheric C-14 is the same today as it was when these dinosaurs were still living (i.e., pre-Flood).

Yet, why make this assumption? Rana mistakenly applies his own “old earth” model to interpretations of C-14 and then suggests this disproves a “young earth” model. In a “young earth, global flood” model, the early atmospheric level of C-14 would almost certainly have been much lower than our contemporary level (Baumgardner, 2005; Snelling, 2009). At the time of their burial by the Genesis Flood, the level of C-14 in dinosaur fossils would have been far less than Rana assumes. Consequently, the amount of C-14 still remaining in these fossils is fully consistent with an age of just a few thousand years.

Furthermore, Rana fails to acknowledge that C-14 is not limited to only a few anomalous dinosaur fossils. Instead, fairly uniform levels of C-14 are found in a variety of fossils, as well as coal, petrified wood, natural gas, oil, and even diamonds (Baumgardner, 2005). This further strains Rana's attempted rationalization for the presence of C-14. Even a combination of his proposed explanations does not adequately account for the consistent and almost ubiquitous presence of C-14 in fossils and other material from different geologic strata all around the world. In fact, his assumptions fall dramatically short of an adequate explanation.

I also find it extremely inconsistent that Dr. Rana would rightly reject the tenets of Darwinism (pp. 85–86) but fail to recognize that the dating methods he ardently defends are heavily based upon those very tenets. He seems completely oblivious to the strong naturalism underpinnings of contemporary dating paradigms (Reed, 2013). Charles Lyell, who was very influential in establishing an early geologic timescale, even admits that a major purpose of his writing was to “free science from Moses” (Lyell, 1881, p. 268).

In addition, radiometric dating was not developed until decades after vast ages were already assigned to geologic strata. These initial dates were based mostly upon a presumed evolutionary history of fossil sequences (biostratigraphy) and a presumed slow sedimentation rate. Evolutionary assumptions figured very prominently into this ideology (Berry, 1987). As a matter of historic record, radiometric clocks were not used to establish the ages for the strata. Rather, the evolution-based ages of the strata were used to evaluate and select appropriate radiometric clocks. Does anyone really believe a radiometric protocol that failed to give the already assigned millions-of-years age would have been considered valid? Thus, “radiometric dating is not an independent verification

of the long age assumption, but is a direct product” of that assumption (Anderson, 2016, p. 50).

Tissue Chemistry

Rana's second major point in *Dinosaur Blood* is that the chemical nature of the tissue could enable it to survive long periods of time. Indeed, not only has collagen been detected in a dinosaur fossil assigned as 85 million years old (Schweitzer et al., 2009), but it has also been reported in a reptile claimed to be 247 million years old (Surmik et al., 2016). Rana writes at length that the chemical structures of various biological molecules (e.g., collagen, keratin, and chitin) make them so structurally “tough” that they can withstand almost any environmental condition (pp. 54–62). From this he concludes that it should not be too surprising that fragments of these molecules may actually survive for millions of years.

However, he fails to provide support for his conclusions with any degradation studies. He merely makes assumptions and inferences that fit his support of the popular timescale. Certainly some biological molecules, such as collagen, degrade at a much slower rate than many other biomolecules. Yet there is no experimental evidence that collagen could survive for 80 million years, let alone over 200 million years. In fact, studies have repeatedly demonstrated that collagen cannot survive for more than a fraction of that length of time (Anderson, 2016; Thomas, 2015). Thus, the conflict of the timescale with the empirical data is evident.

The problem Rana faces is that the experimental decay studies give an upper survival limit for bone collagen at about one million years at normal subsurface temperatures (e.g., Buckley and Collins, 2011). As a rebuttal, he attempts to challenge the validity of these studies by claiming their methodology employed too high of temperatures. He reasons that because high temperatures

will dramatically accelerate protein degradation, these studies cannot be applied to decay rates in cooler environments (p. 68).

Unfortunately, he presents a complete misunderstanding of the experimental methods of these studies. Higher temperatures are often used in decay experiments to accelerate protein degradation. At lower temperatures the degradation will be considerably slower, which could extend the length of the experiment by months or even years. As long as the protein decay rate fits a first- or second-order reaction curve (Collins et al., 1995; Millward and Bates, 1981), the Arrhenius equation enables decay rate conversion between different temperatures. Thus, decay measured at high temperatures can be used to predict the decay rates at lower temperatures. This is a common practice in protein biochemistry.

Rana counters this by suggesting that high temperatures may unexpectedly alter how collagen molecules degrade. Such an unexpected change in degradation prevents the Arrhenius equation from properly predicting decay rates at lower temperatures (p. 68). However, Rana is merely offering speculation. If he wants to seriously challenge the accuracy of these studies, he must offer experimental evidence that high temperatures will unexpectedly alter collagen decay. He must offer counterexperiments showing that collagen decay will not fit the predicted reaction curves. He must also demonstrate that decades of experiments verifying the temperature dependence of equilibrium constants for chemical reactions is actually wrong. In other words, he must offer far more than just conjecture. As a chemist he should know better.

What is more, his intense focus on collagen as the “most likely biomaterial to survive in fossils” (p. 31) apparently caused him to forget all the other proteins that have been detected in dinosaur fossils (Cleland et al., 2015). Many

of these proteins (e.g., hemoglobin, myosin, actin, and tropomyosin) are not nearly as structurally “tough” as collagen. There is no experimental evidence that fragments of all these additional proteins could survive for more than a fraction of the time that collagen could survive.

Schweitzer et al. (2013) suggest that the interaction of actin with α -actinin and fimbrin may help stabilize the protein after cell death. However, it is strictly conjecture that such an interaction would provide stability for millions of years. They offer some studies of cell apoptosis as support for their hypothesis (Schweitzer et al., 2013), but such studies have not provided consistent results regarding actin's degradation rate (Kayalar et al., 1996; Song et al., 1997). Plus, apoptosis is a special, cell-activated process that does not necessarily involve the same cell destruction processes that occur postmortem.

In fact, degradation studies would suggest several of these other proteins degrade fairly rapidly postmortem (Lamestsch et al., 2002; Lamestsch et al., 2003; Wang et al., 2011). Some of these proteins also have high turnover rates in the cell (Seene and Alev, 1991; Theroit, 1997; McGrath et al., 1998), further indicating they are not overly resistant to degradation. Even if Rana thinks there is a biochemical basis for collagen fragments to survive 80 million years, this cannot be said about all of these other proteins.

Rana also lists a variety of environmental conditions that may contribute to tissue preservation. However, he tends to spin in circles. He states that high temperature and high/low pH can inhibit enzymatic and microbial activity, which enhances tissue preservation. Yet he acknowledges that these conditions can also accelerate tissue and protein degradation (pp. 65–66). He states that “sequestering soft tissue from oxygen is another significant preservation factor” (p. 64), but then he admits the presence

of oxygen can help in preservation (p. 64). He states that a water-free environment would help preserve the tissue (p. 63), but he recognizes that water is needed for a fossilization process that facilitates tissue preservation (p. 62). He states that a dry environment provides the best condition for tissue preservation, but he admits some water is needed for prolonged preservation of collagen (p. 64).

He concludes that no single process likely enabled the extensive preservation of the tissue (p. 54). However, he fails to acknowledge that many of the proposed preservation processes offer chemically opposing dynamics. For example, processes that may help preserve collagen can accelerate decay of other proteins. He even cites my challenge that millions of years of exposure to ground radiation would be devastating to the tissue (Anderson, 2015), yet he offers no subsequent rebuttal or counterexplanation (p. 34).

Protein cross-linking, caused by oxygen-derived free radicals, is an integral component of Schweitzer's iron model for tissue preservation (Schweitzer et al., 2014). This model is the fundamental mechanism currently offered to explain the extensively prolonged preservation of tissue, especially blood vessels from dinosaur bone (Anderson, 2016). Yet Rana offers only a superficial discussion of this model (pp. 64–65). In fact, conspicuous by its absence, he does not even mention DeMassa and Boudreaux's (2015) detailed evaluation of this proposed process. Since their article is part of the same special CRSQ iDINO report that Rana possesses, he apparently simply chose to ignore it.

Failure to even attempt a rebuttal of DeMassa and Boudreaux (2015) dramatically reduces the overall weight of his arguments in *Dinosaur Blood*. The other proposed preservation factors that Rana spends page after page discussing are only of secondary importance. Not coincidentally, by failing to devote much

attention to the iron model, he is also spared the need to defend it. Thus, he does not address its numerous chemical flaws, such as the problem that free radical reactions would hydrolytically degrade far more protein than free-radical-induced cross-linking would preserve. Rana takes a convenient position but not a position that should be scientifically satisfying for someone whose professional training is in chemistry.

Ultimately he struggles with explaining the preservation of dinosaur tissue (or tissue from even more “ancient” fossils). Instead, he primarily makes inferences, offering the reader very little experimental data and providing no cogent defense of the iron-preservation model. This is not surprising, per se, as virtually none of the experimental data support his presumptions (Anderson, 2016; Thomas, 2015).

This adds to the irony of Rana’s rather predictable mantra: young-earth creationists offer “bad science” that turns people away from Christianity (p. 74). In the case of dinosaur tissue, evolutionists (and Rana) are scrambling for explanations, offering speculations and conjecture but very little experimental support (Anderson, 2016; Thomas, 2015). The discovery of flexible tissue in a supposed 550-million-year-old beard worm (Moczydłowska et al., 2014) and evidence of trace amounts of protein fragments still retained in a 417-million-year-old arthropod (Cody et al., 2011) stretches the credibility of any preservation mechanism (no matter how fanciful) to the breaking point. Yet biblical creationists are the ones accused of engaging in “bad science.”

Final Point

Rana defers to popular opinion as evidence for his position (a common tactic used against biblical creationists). He observes that “few people in the scientific community are impressed with this latest argument for a young earth” (p. 11). From this, he concludes that the

“young earth” claims regarding dinosaur tissue are not very strong.

I find it rather ironic that he would make such a comment when it almost equally applies to his own viewpoint. Rana’s ideas of progressive creation—with arbitrary sprinklings of creation miracles scattered across great lengths of time—is no more popular within the scientific community, at large, than that of a recent creation. Which mainstream science journals “sing the praise” of progressive creation (or theistic evolution, for that matter)? Does popularity become important only when it agrees with his particular argument?

Furthermore, scientific interpretations should never be based upon popular vote. No type of truth or understanding should depend upon its popularity. In fact, there are many instances in the history of science where an unpopular view eventually proved correct. As a young scientist my postdoctoral advisor and I proposed a rather unpopular idea about bacterial metabolism that was eventually accepted as the correct explanation (Koropatkin et al., 2008). The early unpopularity of our idea was not an indicator of whether it was correct.

Nor should Christians ever be concerned about what a fallen world accepts as truthful or factual. Jesus warned that many are on the path that leads to destruction, while only a few are on the path to righteousness (Matthew 7:13–14). In such a corrupt world, would we seriously expect evidence for a creator or for a “young” earth to be widely embraced? Even the scientific community is hardly immune to the effects of this “fallen world” as the influence of a materialistic worldview becomes increasingly entrenched.

The dilemmas of Howard Van Till and Davis Young should serve as a clear warning. Decades ago both were highly influential advocates of an “old earth” understanding of Genesis. Both originally promoted some type of non-literal view of Genesis 1, not unlike

the “day-age” view that Rana argues for in *Dinosaur Blood* (p. 80). Both have subsequently abandoned such an interpretation and have determined that Genesis 1–11 has no factual or historical value. Young now writes for the evolutionist group BioLogos, and Van Till holds views more consistent with deism. Both unsuccessfully teetered on the same “slippery slope” where Rana is asking all of us to stand.

I have numerous books in my library in which the authors explain how they came to accept the popular teachings of the earth’s age as a first step toward atheism. Interestingly, one of these authors even points to reading a book by Van Till as one of his first steps. In contrast, I am not aware of anyone accepting the less popular “young earth” position as a first step toward atheism.

Rana wrote *Dinosaur Blood* for the apparent purpose of trying to blunt the implications of the dinosaur tissue discovery. Interestingly, the contradictory and speculative nature of his arguments reveals the difficulty this discovery presents to the standard geological timescale. He is unable to present cogent and consistent reasoning. Instead, he glosses over or even avoids key concepts and frequently offers conjecture rather than supporting experimental data.

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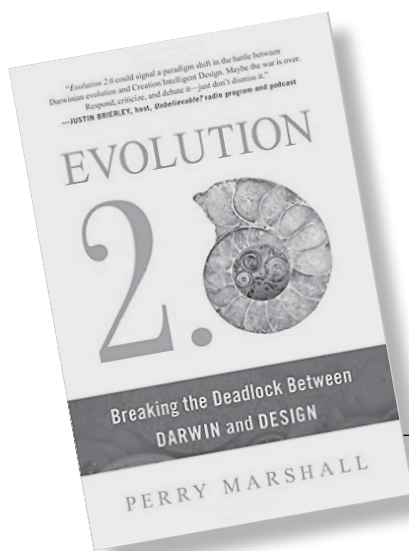
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Evolution 2.0: Breaking the Deadlock Between Darwin and Design

by Perry Marshall

BenBella Books, Inc., Dallas,
Texas, 2015, 374 pages, \$24.95

Evolution 2.0 is an interesting book—at times quite lucid and convincing, but at other times contradictory and confusing. There are several well-written chapters with novel ideas, but these are mixed with other sections that seem illogical.

Author Perry Marshall's basic thesis is that both neo-Darwinism and intelligent design are wrong. Instead, he says, *Evolution 2.0* is a “third way” of interpreting the evidence. *Evolution 2.0* is defined as “the cell's capacity to adapt and to generate new features and new species by engineering its own genetics in real time” (p. 145). Marshall envisions the process to work by five mechanisms:

1. Transposition (jumping genes; cells swapping parts of their DNA to adapt to their environment)

2. Horizontal gene transfer (cells exchanging DNA and editing their own genomes)
3. Epigenetics (cells switching genetic code on and off as the need arises)
4. Symbiogenesis (cells or organisms merging to create a new life-form)
5. Genome duplication (hybridization; two species combining to form a new species)

Marshall says that mechanisms 1, 2, and 3 can explain small-scale change (adaptation or microevolution). This (to me at least) is not particularly controversial. These processes provide means by which cells/organisms can sense their environment and adapt quickly to changes by swapping or mixing of genetic material.

Mechanisms 4 and 5 are said to explain large-scale changes (macroevolution). Marshall claims that “new

organelles, bodies, organs, and species arise from symbiogenesis” (p. 130) and that genome “duplications fueled sudden, radical transformations of body plans” (p. 135). He proposes that these mechanisms “explain why the fossil record so often shows a series of sudden jumps” (p. 125). *Evolution 2.0* is said to bring about macroevolution without invoking neo-Darwinian pathways. The trouble with this claim is that there is little (if any) evidence that mechanisms 4 and 5 can produce the radically new body parts and plans that macroevolution would require.

Marshall accepts universal common descent and a 3.5-billion-year history of life on Earth, but he rejects the neo-Darwinian mechanism of random mutation and natural selection. In essence, he believes that sufficient biological information was built into life from the

beginning and that both micro- and macroevolutionary change can be explained by the Evolution 2.0 mechanisms. Marshall does a nice job of attacking and destroying neo-Darwinism, but his alternative (at least for macroevolution) is far from convincing.

Marshall draws from his engineering background to craft a nice section on biological information and noise. He states that “random mutation is noise, and noise destroys” (p. 71). Marshall’s belief in common descent seems somewhat inconsistent with the notion of biological “noise.” Marshall states correctly that “DNA copying errors trigger a species’ decline” (p. 74), in which case one might think that after 3.5 billion years of evolution, life would be extinguished by accumulated mutations (noise). Marshall apparently gets around the decline-of-fitness issue by citing the cell’s ability to correct errors: “Any life form without the ability to repair DNA copying errors would fast perish” (p. 187). However, it is well known that copying errors (and other mutations) do accumulate over time. Marshall mentions “information entropy” as a synonym for noise, and this seems to be equivalent to J. C. Sanford’s term “genetic entropy” in his *Genetic Entropy and the Mystery of the Genome* (Sanford, 2005). Marshall includes a reference to Sanford’s book, but he apparently failed to heed the book’s message of declining genetic fitness over time.

Marshall promotes Evolution 2.0 as a new unifying concept, but in reality his ideas are not new. For example, microbiologist James Shapiro (Shapiro, 2011) describes essentially the same concept, which he calls “natural genetic engineering.” While Shapiro and like-minded colleagues reject neo-Darwinian theory, they are all naturalistic

evolutionists who view the new concepts as purely material in nature.

Marshall’s views also have some similarity to Lee Spetner’s “nonrandom evolutionary hypothesis” (or NREH; Spetner, 2014). The NREH includes Marshall’s first three mechanisms (for adaptation). Spetner does not endorse common descent, however, and his book does not mention Marshall’s mechanisms 4 and 5.

Interestingly, Marshall is not a materialist but rather a type of theistic evolutionist. He states that “the origin of life has all indications of being a deliberate, astonishing act of outside intelligence – a miracle, you could say” (p. 219). Marshall says that DNA “is a code, a language, and an information storage mechanism” (p. 192), and “all we observe about the creation of codes directly implies a designer” (p. 184).

In an appendix called “Genesis 2.0,” Marshall invokes a “day-age” interpretation of the Genesis Creation account. He accepts big bang theory and an old Earth. Marshall states that science supports the Genesis order of appearance of life-forms (plants followed by simple animals, then more complex animals, and finally man). Genesis “days” are not literal, in his view but instead are ages or eras of long duration. Marshall believes we are still in Day 7 and that no new life-forms are being created. In many ways Marshall’s interpretation of Genesis is similar to that of old-earth creationist Hugh Ross (Ross, 2004).

Marshall’s book criticizes both young-earth creation (YEC) and intelligent design (ID). He says YEC “runs into trouble with the speed of light and radiometric dating, plus astronomy, geology, and a half dozen other disciplines” (p. 308). Marshall states that “ID too quickly jumps to ‘Designer’ as an immediate explanation” (p. 213) and that

“ID pits faith against science” (p. 213). Such naive statements indicate that Marshall does not understand YEC and ID concepts very well and that he is echoing typical criticisms that have been levied by others. In essence, Marshall endorses many creation and design concepts, but he doesn’t want to be associated with those terms.

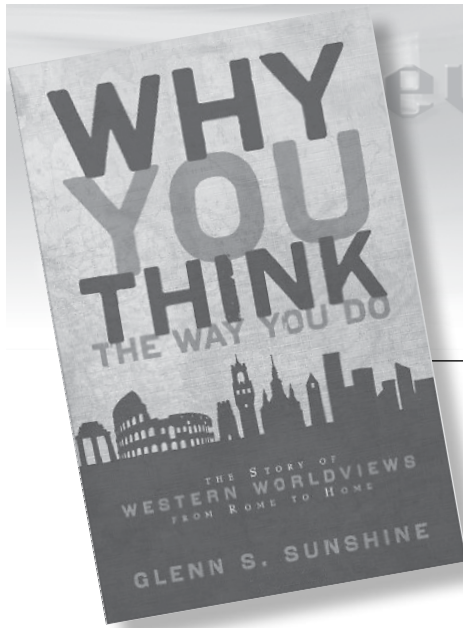
I do think that Marshall’s book provides a good take-home message for creation and design proponents. While we have been busy fighting neo-Darwinism, we should realize that many mainline evolutionary biologists are also seeking to replace the random mutation/natural selection paradigm. We should be cognizant that while neo-Darwinism is in decline, its emerging replacement (natural genetic engineering) is also a form of naturalistic, non-teleological, unguided evolution.

While Evolution 2.0 encompasses essentially the same mechanisms as natural genetic engineering, Marshall at least acknowledges that the Creator is responsible for the original design—including the genetic code, biomolecules, cellular structure, and adaptation mechanisms that make life possible. In that sense he is a creation/design proponent, whether he cares to admit it or not.

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Why You Think the Way You Do: The Story of Western Worldviews from Rome to Home

by Glenn Sunshine

Zondervan, Grand Rapids,
2009, 240 pages, \$15.00

This book is required reading in the Centurions Program, also called the (Charles) Colson Fellows Program. It is an intense yearlong study with 12 book readings, eight classic films reviewed, written white papers, and seminars held at the Colson Center in Lansdowne, Virginia. The goal is to encourage a solid Christian worldview so that participants can navigate the changing culture and help reshape it in a way pleasing to God. Worldview is defined as “the framework you use to interpret the world and your place in it. It is like a set of glasses that you look through to bring what is happening in the world into mental focus” (p. 13).

Everyone has a worldview even if not aware of it. Personal answers to four basic questions frame this worldview: *Where did I come from? What is wrong with the world? What is the solution? What is my purpose?* At a deeper philosophical level, one may consider what is real (metaphysics), what is truth (epistemology), what is right (ethics), and what is good (aesthetics). Author Sunshine (one simply must smile at the optimistic name)

shows familiarity with minute details of Greek, Roman, Medieval, and Renaissance history. Every page connects history with multiple names, both familiar and obscure.

The author is professor of history at the Central Connecticut State University. Because he has no particular connection with the creation worldview, Sunshine’s challenges to evolution are especially encouraging. Darwinism is challenged as not amenable to testing by the scientific method: “The past is over; you cannot revisit it, observe it, test it, or experiment on it. All you can do is look at the surviving evidence and try to make sense of it” (p. 167). Also, as a denial of macroevolution, “You can take a goldfish and give it eyes that protrude, change its color to black, and divide its tail, but you cannot turn a goldfish into a goldfinch” (p. 167).

Sunshine further challenges evolution adherents with the question, “What evidence would falsify Darwinism? If you cannot think of or imagine anything that would, it is an article of faith and not a scientific theory” (pp. 168-169). What Sunshine means is that any data that discredits Darwinism is explained away, including the mystery of the spontaneous origin of life, the Cambrian explosion of life, and the complexity of trilobite fossils.

The latter half of the book challenges substitutes for biblical theism. These failed worldviews include various world religions, modernism, postmodernism, eco-spirituality and a dozen more. Regarding ethics, naturalists are pictured as having “their feet planted firmly in midair” (p. 172). The book had me reaching for a dictionary for the meaning of terms such as *antinatalism*, *Ciceronians*, *dialectical materialism*, *Jansenism*, *polyandry*, *polyamory* and *Pyrrhonism*. This is a positive comment for the book, which is filled with insights into our Western mindset.

The book has a serious conclusion. The case is made that the identical cultural shifts that brought down the Roman Empire are developing at lightning speed in the West, including the U.S. The shifts include widespread abortion, denial of absolute truth, paganism, promiscuity, required acceptance of antibiblical lifestyles, slavery via human trafficking, and more. All this justifies the importance of the Centurions Program, along with an army of people with mature Christian faith. The book has full references along with name and subject indexes.

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One Small Speck to Man: The Evolution Myth (2nd edition)

by Vij Soderá

Vij Soderá Productions, UK,
2013, 562 pages, hardcover,
\$55.00

This greatly enlarged and updated edition of Dr. Vij Soderá's book is one of the most compressive compendiums on the many problems with Darwinism. This edition has 17 new sections, 100 new pages, and 600 new photographs. Vij Soderá, M.D., a fellow of the Edinburgh Royal College of Surgeons, has had an interest in animal biology since a youth.

Soderá effectively catches the reader's attention with his lively discussions in 562, 8.5-by-11-inch pages. The glossy-paper hardbound book has over 800 full-color photographs, diagrams, and paintings. The anatomical dissections, most of the photography, and all the artwork and diagrams were drawn by Dr. Soderá. The author, an accomplished wildlife artist, has exhibited and sold many of his paintings.

Although he was taught only evolutionism in his high school and university training, Dr. Soderá's own research has caused him to conclude that the theory is based on very tenuous and unconvincing evidence. This book is the result of his almost 30 years of rigorous research on the scientific evidence for biological origins. In the text, Dr. Soderá attempts to answer this question: Is it possible that simple molecules will, after a few billion years, bond with other simple molecules and eventually acquire consciousness—to ultimately peer down on other molecules and contemplate its origins?

Inherent in the theory of evolution by natural selection is the assumption that not only is macroevolution possible but also that evidence exists that it actually happened. Orthodox Darwinism claims that simple molecules dissolved in water became living cells without any outside influence. Some of these cells eventually became fish, others amphibians, reptiles, birds, mammals, and monkeys, and others became you and me. Dr. Soderá stresses that only by objectively evaluating all of the evidence and being willing to challenge established dogma can we hope to understand reality.

This encyclopedic volume provides a detailed, well-documented, up-to-date discussion of the major scientific problems with macroevolution. It provides extensive and compelling scientific evidence that macroevolution did not occur and could not have occurred. Dr. Soderá looked only at the empirical data and based his conclusions only on this data. The many topics covered include coelacanths, human-ape fossils, embryology, dinosaurs, muscle contraction, sedimentary rocks, mass extinctions, genetic variation, molecular biology, DNA and protein, molecular machines, the eye, the fossil record, the human upright gait, the mind, plus whale, elephant, snake, and bird origins.

One strength of the modern creation community that is now reevaluating macroevolution is the large variety of people from many countries and diverse scientific disciplines that are contribut-

ing to the research. This book, with its many original arguments, is one more of many examples of this literature.

Dr. Soderá's natural history research has taken him to Africa, Canada, and Iceland, where he has studied and photographed diverse forms of wildlife. His travels have contributed to his lifelong work in the field of biological origins that are reflected in his book. Dr. Soderá's medical skills and interest in anatomy, physiology, and biochemistry have also enabled him to research in detail evolutionary arguments, especially in the fields of paleontology and biology. He has gathered and evaluated the relevant data necessary to analyze Darwinism in light of the principles he has derived from his experimental and field research.

Among the new principles he developed that he has applied to evolution is the Chalicotherium principle. This principle is that the specific morphology of a body cannot be determined from teeth or skulls alone, as macroevolution has often attempted to do. Chalicotherium was an extinct animal that had a skull much like a horse, a body similar to a sloth, and arms like a gorilla (pp. 204–205). This example shows that historical evolutionary relationship cannot be proven solely on the basis of teeth or skull similarity.

Another example—the Coelacanth principle—was named after a fish once claimed by evolutionists to be an important evolutionary link. Scientists

were forced to totally reevaluate their evolution theories when living specimens of a fish widely believed to have become extinct about 70 million years ago were discovered in 1938. Dr. Soderá concluded from this and other evidence that in the absence of direct evidence to the contrary, any creature could have lived at any time before or after the time of its earliest or latest known fossil, an argument that helps us to view the fossil record in a very different light than that of many contemporary evolutionists.

Furthermore, the existing fossil record is a composite artifact: all types of creatures (both living and extinct) could have lived contemporaneously in prehistoric times, and there is little empirical evidence for the generalization that organisms have become increasingly complex over time. Furthermore, the high level of morphological constancy over time manifested by many creatures is evidence against an animal kind having lived millions of years ago. Dr. Soderá also concluded that under very favorable conditions some fossils can be formed in less than a year.

Dr. Soderá's original approach allows him to occasionally interpret artifacts differently than other specialists. For example, he suggests that Archaeopteryx was a feathered dinosaur because of its many reptilian features and the lack of a supracoracoideu pulley system. Otherwise, it was very unlike any other known bird. Furthermore, a step-wise evolution of the bird supracoracoideu pulley system is very implausible (p. 248).

Soderá shows in the chapter on eye evolution that many different eye types

exist in animals, but no pattern exists that supports an evolutionary trend. For example, vertebrates from the most primitive bony fish to the most advanced humans show much variety but no evidence of evolution. The so-called least evolved "lowest" vertebrate eye type is not less complex than the human eye, just different. Design modifications were made only to enable the animals to live in its normal environment. Another example is animals thought to be very primitive, such as sharks, have advanced design features that are absent in so-called more advanced animals.

Other principles that he has developed includes the disuse principle (disuse alone will usually not cause degeneration of a structure), the intermediate principle (more intermediary fossil types should normally exist than non-intermediate, although more non-intermediate examples may exist), and a statistical argument called "What You Want You Won't Get" (WYWWG), meaning it is unlikely that an animal will acquire the specific mutations needed to evolve into more complex life-forms.

Some Background of the Author

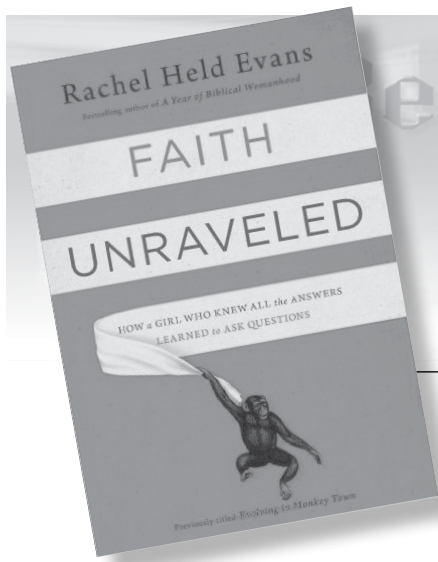
Dr. Soderá was born in India and has lived in England since age four. After earning major school prizes for academic and art achievement at St. Clement Danes Grammar School in London, he graduated from Sheffield University Medical School with distinction in chemistry and became a fellow of the Royal College of Surgeons in 1981. During the over 25 years he has

practiced medicine, Dr. Soderá has authored three extensively illustrated, acclaimed medical textbooks (*Skin Surgery in General Practice: A Diagnostic Atlas*, *Minor Surgery in Practice*, and *Illustrated Handbook of Minor Surgery and Operative Technique*) with sales of over 15,000. Dr. Soderá is currently working on two new surgery textbooks. He also regularly publishes articles in the scientific literature and is planning a television series based on his book *One Small Speck*. He also has produced two DVDs— one on human fossils and one on the impossibility of macroevolution.

Although the cost of *One Small Speck* is equal to that of two average books, it has four times the text and hundreds of color photos—important because a picture is worth a thousand words. For a detailed critique of evolution theory (especially concerns relating to the anatomy and physiology of living and extinct animals), this book is an excellent investment. It is highly recommended for high school and college level readers interested in science, as well as church and school libraries as a reference for interested persons.

This outstanding work is the only book of its kind and provides unique insight into the living world. It includes an index, and all of the quotes are documented, most from academic books. Citations from current textbooks are often used because the focus is on students, and original papers on issues that are particularly important are referenced.

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Faith Unraveled: How a Girl Who Knew All the Answers Learned to Ask Questions

by Rachel Held Evans

Zondervan, Grand Rapids,
2014, 232 pages, \$15.00

Eighty years after the Scopes trial spectacle that brought national attention to her hometown, Rachel Evans began to doubt her own faith. She grew up with the many advantages of Christianity, including a Christian home, private schooling, a theologian dad, and her school's "Best Christian Attitude Award" for four consecutive years. Although she grew up in a culture she claims was obsessed with apologetics, Evans asked a lot of questions that indicated that she had very inadequate training. She writes that she "used to be a fundamentalist in the sense that I thought salvation means having the right opinions about God and that fighting the good fight of faith requires defending those opinions at all costs" (p. 17).

After she was exposed to Darwinism, she learned that in order for her faith to survive, she must adapt (actually conform) to biological evolution. Using as an illustration of her own spiritual journey from certainty, through doubt, to a "modern" Darwin faith, Evans illustrates the ongoing dialogue about the church that has captivated the Christian community in recent years.

This book is the story of her loss of creationist belief, as well as the basic Christian doctrines. Evans achieved a tremendous amount of positive publicity for her book, including a positive

article in USA today. The book garnered a whopping 174 reviews on Amazon, almost all very laudatory, with only 1% giving it a poor rating.

Evans's harsh judgments of the Christian worldview in which she grew up results in her cynicism pervading the book's narrative. She claims that she was taught at Bryan College that evolution fails to account for the enormous complexity that is "inherent in biological organisms, to produce a sufficient fossil record of transitional species, and to explain the many ambiguities in biological classification. Therefore, it should not be taught as fact in public schools. Most important, the theory of evolution is dangerous because it undermines the authority of the Bible and threatens the foundation of Christianity" (p. 70).

All of this she says, she has now rejected, including what she learned "from Dr. Kurt Wise, one of the leading young-earth creationists in the country and a favorite professor among Bryan College students. ... Armed with a degree in paleontology from Harvard University, Dr. Wise had studied under Stephen J. Gould, a renowned evolutionist and science writer. Dr. Wise said that his goal was to formulate a model of earth history consistent with both Scripture and the scientific data" (p. 70).

She adds that in "many ways, Dr. Wise embodied the spirit of Bryan College. While not everyone on campus supported young-earth creationism, the overriding principle behind the school's educational approach was that the Bible serves as our most reliable textbook, that

it provides an infallible foundation on which to build the academic disciplines.

From that foundation students "learned that everything from science to history, economics, art, psychology, politics, and literature can be studied from a biblical worldview" (p. 71). She would soon also reject all of this, and her lack of knowledge shows when she tries to explain why. As an example, she naively asks, "What if Galileo had simply accepted church-instituted cosmology paradigms?" (p. 219). She obtained much of the information that caused her to accept evolution from the mass media, admitting that one of her favorite TV series of all time was BBC's very biased series on evolution titled *Planet Earth* (p. 210). She loved the show because narrator David Attenborough "shows how magnificently living organisms can adapt to their environments. From the extra-thick eyelashes of the wild Bactrian camel, to the dense white fur of the Arctic hare, to the sticky yellow toes of the gliding leaf frog, each animal has its unique way of thriving in its habitat, be it a dusty desert, a snowy tundra, or the tops of trees" (pp. 210–211). This evidence is hardly proof of Darwinism.

The next evidence she cites in favor of evolution concerns cave angelfish. She notes that marine angelfish are known for their colorful fins and attractiveness in aquariums, but because cave angelfish "lost the pigment in their skin, they look more like ghostly, winged snakes than fish. Microscopic hooks on their fins allow them to cling to cave walls like bats. Positioned just

right, they can feed on bacteria rushing down the waterfalls. Their eye sockets are empty, their bodies elongated and slimy” (p. 211).

Her arguments for evolution include that evolutionists “*believe* that a group of marine angelfish *must* have migrated to the caves millions of years ago to escape predators or to adjust to climate change. Like many cave dwellers, over the years they evolved blindness and improved other sensory functions because in their environment eyesight was no longer useful. Cave angelfish live exclusively in a few remote caves in Thailand, and the *Planet Earth* crew went to all kinds of trouble to capture footage of these little survivors in their natural habitat” (p. 211, emphasis added). Loss of function is not a problem for creation, but the gain of function is a major problem for evolution.

Evans also learned evolution from

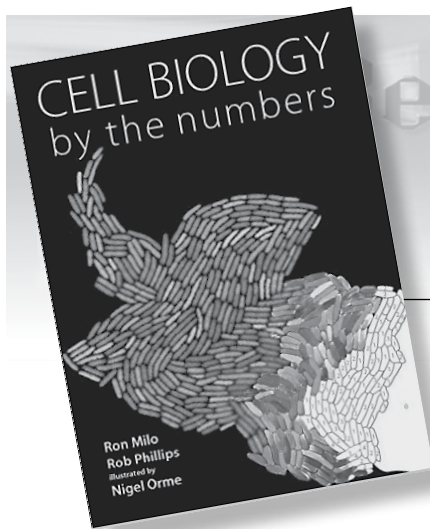
the social-media, hardly a source of solid scientific information. In one blog she “encountered all kinds of people, young and old, who no longer considered themselves Christians because of false fundamentals” such as one person who “took a biology class and was convinced that the theory of evolution was sound,” and another who opined that she is “tired of fighting the culture wars” (p. 208). She adds, “I looked into the science behind evolution” (p. 97) and asked “why are we so afraid to confront the mountain of scientific evidence in support of evolution?” (p. 96).

Evans admits that her experience at Bryan College “was everything a college experience should be. I made lifelong friends, learned how to think critically, and became well versed in Christian apologetics” (p. 78). However, as is obvious from her writings, she was *not* very well versed in Christian apologetics.

Other things she claimed occurred at Bryan College included that Christians “accused scientists of having an agenda, of ignoring science that contradicted the evolution paradigm, but engaged in some mental gymnastics of our own, trying to explain how it’s possible to see the light from distant stars” (p. 79).

Evans admits, “My story isn’t pretty,” and it isn’t finished yet, but she is “telling it because it’s the best evidence I’ve got in support of ... evolution.” Concluding that Christianity must adapt to Darwinism (p. 212), she never hints at the so-called mountains of evidence she claims exists for evolution. This book is an eloquent example of what happens when one’s heart is poorly grounded in the evidence against Darwinism and for creation.

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Cell Biology by the Numbers

by Ron Milo
and Rob Phillips

Garland Science, New York,
2015, 400 pages, \$49.95

Many interesting works focus on the intense debate between biblical and secular humanistic worldviews and how they interpret origins, revolving around the evidence supporting each position. This book isn't one of them. Rather, it takes the reader on a fascinating expedition into the microscopic world of the cell. The authors have compiled information from many researchers that address cellular questions about how big/how much/how fast/how strong and put these questions into perspective as to what a cell is all about. While not strictly origins-oriented, the incredible complexity displayed in my opinion speaks strongly of the existence of an omniscient, omnipotent Creator who designed the cell, the fundamental building block of all life.

Authors Milo and Phillips rely on two basic approaches in this text: first, reference to an extensive compilation of biologically measured numbers as archived on the BioNumbers website (<http://bionumbers.hms.harvard.edu/>), and, second, on the ability to use “back of the envelope” estimations and calculations to make sense of these numbers. The book begins with a lengthy description of these approaches. One can become adept at “street-fighting cell biology” (p. xlii) and make critical evaluations of the validity of different numerical claims, even given the fact that very few biological numbers are

absolute but vary under differing growth conditions, cell state, etc. In other words, does a specific claim make sense in comparison to what is known about the world of the cell?

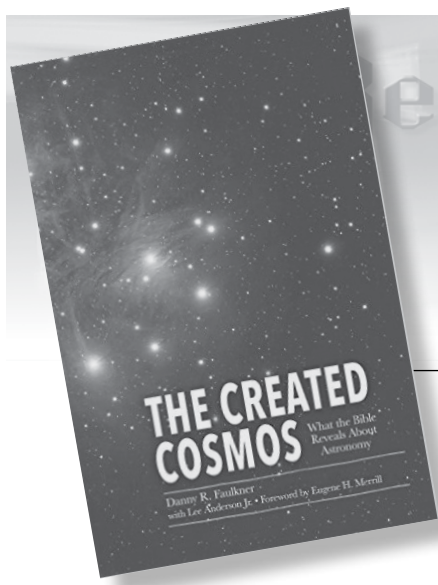
The bulk of the book is composed of a series of vignettes, each examining a different question about basic cell biology such as, “What is the macromolecular composition of the cell?” and “How many ions pass through an ion channel per second?” These are generally organized into chapters focused on size, concentration/absolute numbers, energy/force, rates, and cellular information. Many of these vignettes contain absolutely amazing information that points to the complexity of life (and, to me, the greatness of the Creator). As examples, if a bacterium were the size of you, then a yeast cell would be the size of an elephant, and a human cell would be the size of a blue whale (pp. 13, 17). An activated B cell secretes its weight in antibodies every day (p. 28). Also, 100 gigatons (10^{11} tons) of CO_2 are fixed by photosynthesis every year (p. 45). If DNA were scaled up to one meter in diameter, the replicase copying would be the size of a FedEx truck, driving along the DNA at 600 km/hr and delivering 1000 DNA base “packages” per second, while making a delivery mistake only once every few hundred kilometers (p. 51). Movement by diffusion inside cells is very rapid. In a bacterium, a positive charge jumps among its 2×10^{10} water molecules rapidly enough to reach every water molecule about 10 times a second (p. 90). And small molecules will randomly bump into every protein in that same bacterium every second (p. 220). The most

abundant protein on the planet appears to be collagen, with enough material for each of the 7+ billion humans to receive 13 kg of it (p. 111). If human skin were photosynthetic, it would produce about 10 watts of power, $\sim 1/10^{\text{th}}$ of our energy needs (p. 169). Nerves transmit impulses at up to $\frac{1}{2}$ the speed of sound (p. 251). Each one of your cells contain ~ 2 meters of DNA packed inside the nucleus (p. 285). The average human body contains ~ 37 trillion cells, $\sim 85\%$ of which are red blood cells (p. 316).

These facts are almost exclusively presented without any reference to an evolutionary worldview. A reference is made to all life originating in the sea (p. 41) and to the assumption that human chromosome 2 is the result of the fusion of 2 ancestral chromosomes that are still separate in the chimp (pp. 289-290). Mutations are seen as the “highly acclaimed chisel with which evolution sculpts organisms” (p. 297). But even when referencing evolution, the authors also acknowledge the mind-blowing complexity of the cell, citing examples that provide “a dazzling display of subtle and beautiful mechanisms” (p. 182).

While this work is not directly related to the origins debate, the amazing complexity that exists in a “simple” cell is clearly evident through the vignettes presented. It does help to have a background in biology, but even for the casual reader, the picture these authors paint of the cell serve as a great reminder of Psalm 139:14, giving the reader many opportunities to praise the Lord.

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The Created Cosmos: What the Bible Reveals about Astronomy

by Danny Faulkner
and Lee Anderson

Master Books,
Green Forest, AR, 2016,
331 pages, \$20.00

This book exegetically explores astronomy by starting with biblical texts and applying them to diverse questions and beliefs common today. The book is divided into four sections: explicit biblical references to astronomy, anomalies in the Scriptures regarding astronomy, common current astronomy questions that the Bible does not directly address, and theories that claim biblical support. Moving from clear biblical teachings to unclear territory, Faulkner's goal is to equip the reader with information needed to reveal and correct an improper understanding of astronomy while also using Scripture to reinforce truth.

Lee Anderson writes the first chapter and the appendix. I appreciate Anderson's reminder that God's glory and majesty are reflected in creation, especially the cosmos, because it sets a great foundation for the rest of the book. Faulkner recalls this in his own way later in the book when making the case that God is not restricted by laws of

the universe because God is capable of miracles. I love that a strong believer in physics believes the Bible when it claims miraculous actions of God, even when they appear to defy science.

Faulkner's background in education greatly influences *The Created Cosmos*. His writing style exemplifies how to compare and contrast, how to analyze data and how to come to logical conclusions. Unlike some teachers, Faulkner clearly and fairly explains theories and ideals that he disagrees with so the reader will gain understanding and come to a personal position on the issue. He defends his own beliefs with clear explanations. While Faulkner does not preach at the reader, he blatantly disagrees with theories and ideas, especially when he believes they are unbiblical. I respect how he is willing to stand for what he believes but admit when he does not have an answer. When that happens he steps back to cling to what we know without doubt (i.e., Chapter 11), which is a great example for Christians to stay united over the commonality found in Christ alone.

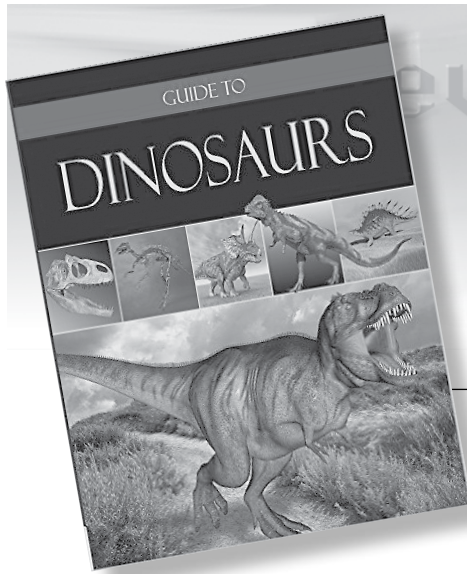
Faulkner defines terms, explains concepts, and writes in a clear, compelling way. He includes dates, names, and

events, which reflects his knowledge of these issues. Occasionally I was lost because Faulkner went into so much depth.

This book is well worth your time because it will help educate you on different ideas present in the world today regarding what the Bible has to say about astronomy. *The Created Cosmos* helped me realize there are a lot more questions about biblical astronomy than I previously thought. Because I have read this book, I will be better prepared to hear and respond to questions that are raised from others and will have a resource to recommend to them.

Danny Faulkner has been studying astronomy for half a century, has graduate degrees in physics and astronomy, and taught for over 26 years at the University of South Carolina Lancaster, where he received Distinguished Professor Emeritus. He currently works for Answers in Genesis and is a member of the Creation Research Society and the editor of the *Creation Research Society Quarterly*.

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Guide to Dinosaurs

by Brian Thomas,
Tim Clarey, Susan Wilson
and Jayme Durant

Harvest House Publishers,
Eugene, OR, 2015, 117 pages,
\$20.00

This full-color illustrated book is written by several Institute for Creation Research (ICR) staff. It is comprehensive in covering dinosaur creation and varieties, the history of their fossil discoveries, their post-Flood Ice-Age challenges, and more.

To give the flavor of the discussion, I will list ten topics that stood out. First, the authors take up the discussion of whether there was pre-Flood rain, suggesting there was none, with an interesting argument. There is evidence that the pre-Flood atmosphere was rich in oxygen, as much as 30% compared with today's 21%. With the early higher value, "lightning would have caused raging forest fires if they'd had storms like we do today" (p. 17). Second, a novel suggestion is given for the significance of Genesis 10:25, when "the earth was divided" during the time of Peleg. The event may refer to the land divided by rivers of melt water, "signifying the end of unstable Ice Age weather patterns" (p. 17).

Third, there were an estimated 60 "kinds" or families of dinosaurs, which

would total 120 on board the ark, including males and females, mainly juveniles (pp. 18, 112). Meanwhile, there are about 25,000 species of land animals living today, including mammals, birds, amphibians, and reptiles (p. 19). Fourth, three-toed dinosaur footprints were found in New England in 1802, the first in North America (p. 39). The book does not discuss their original interpretation as belonging to a large bird, even perhaps "Noah's Raven," a reference to Genesis 8:6–7.

Fifth, as a challenge to geologic "deep time," there is mention of carbon-14 found in diamonds. No mention is made of the creationist RATE project, which publicized this finding. However, references are intentionally kept to a minimum throughout the book. Sixth, there is discussion of the alleged transition of dinosaurs to birds. Multiple problems are listed, including the anatomical changes required: "At some point in its journey, the evolving dinosaur would have lost its ability to walk!" (p. 61).

Seventh, the vegetarian theropod named *Gallimimus* gives evidence in its leg bones of being able to run up to 50 miles per hour (p. 73). If this speed is accurate, it puts the dinosaur in the running for second place for non-flight behind the cheetah. Eighth, there

has long been discussion of the fire-breathing description of the leviathan in Job 41:19–21. The authors comment, "It is possible that some dinosaurs like *Dilophosaurus* could spit venom or even some type of 'fire'" (p. 78).

Ninth, a summary is given of the controversy over the renaming of *Brontosaurus* to *Apatosaurus* (p. 90). Since publication, the debate has been reopened and the name *Brontosaurus* restored (Tennant, 2015).

Finally, a tenth book emphasis is the evidence for rapid Flood burial of many dinosaurs. "Scientists have found evidence of over 10,000 *hadrosaur* dinosaurs buried in one location in Montana" (p. 109).

The book has hundreds of clear illustrations and a concise index. ICR is to be commended for this quality exploration of the dinosaur world.

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References

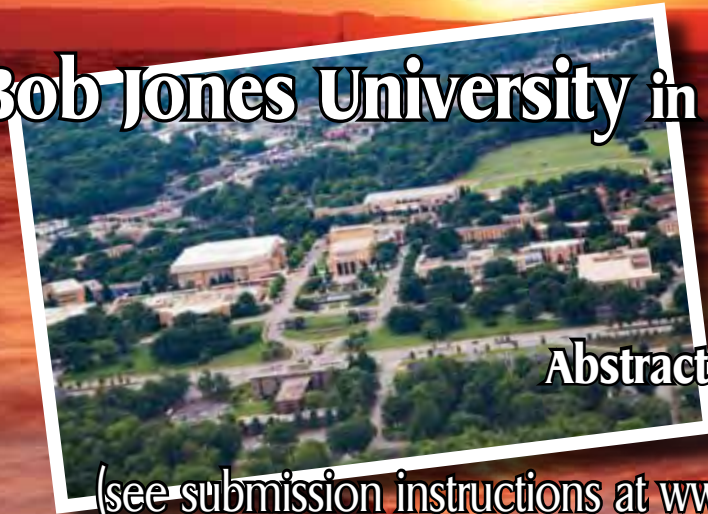
- Tennant, J. 2015. *Brontosaurus* is back! New study finds they aren't *Apatosaurus* after all. Discovermagazine.com, <http://blogs.discovermagazine.com/d-brief/2015/04/07/brontosaurus-is-back/#.VnSzLPkrLIU>.

Creation Research Society Conference

Creation Research Society Conference

July 28–29, 2017

Bob Jones University in Greenville, SC



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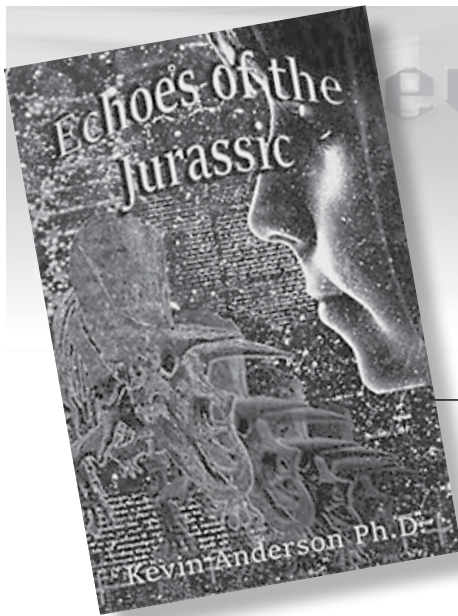
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Reviews

Echoes of the Jurassic

by Kevin Anderson

Creation Research Society
Books, Chino Valley, AZ, 2016,
56 pages, \$6.00

While gutting the West and denigrating the “irrational superstitions” of Christianity, secular intellectuals have waxed lyrical about their open-minded rationalism and empiricism. One creation movement success has been to unveil the hypocrisy, demonstrating that opponents ignore, deny, or distort any evidence that threatens their ivory worldview. Kevin Anderson contributes to this effort with a helpful summary of an ongoing paleontological bombshell—the presence of soft tissue in dinosaur fossils. In a sane world, such a finding would negate deep time and the geological timescale, but it is clear we no longer live there.

A faith commitment to deep time is understandable from a psychological viewpoint. Deep time was the vanguard of “scientific” attacks on Christianity, undermining trust in God’s revelatory truthfulness and in His immanent working in the created order. It remains—in the form of the geological timescale—a significant challenge to Christianity, but one that is vulnerable. Among many, it remains an article of fanatical devotion, justifying their headlong flight from the God that does not exist.

Anderson catches all of these nuances in his concise book, *Echoes of the Jurassic*, published by the Creation Research Society through its iDINO research project. Springboarding off secular work pioneered by Mary Schweitzer over the last decade, Anderson succinctly summarizes the state of soft tissue preservation and documentation in fossils, focusing on a “68-million-year-old” *Triceratops* horn excavated from the Hell Creek Formation in Montana.

Schweitzer found collagen and osteocytes, with remarkable cellular preservation, to the point that proteins and amino acid sequences were examined. SEM photos of osteocytes found by the iDINO project team show the remarkable preservation of the delicate filipodia of these structures. Other studies appear to have found remnants of dinosaur skin, blood vessels, red blood cells, and, more incredibly, chitin preserved in fossils dating back to the Cambrian. It is even possible that DNA may be soon documented in ancient fossils.

Needless to say, these finds invalidate either the timescale or our understanding of biological decay rates and processes in the rock record. If the latter, then *observed* processes and rates (the supposed basis for scientific extrapolation over time) are not relevant to ancient remains. In response, scientists have scrambled for possible mechanisms that would allow such unusual preserva-

tion. One of the strengths of this book is laying out and rebutting the proposed hypotheses of desperation. These include (1) the absence of oxygen or microbes—an unrealistic combination in the cases of the specific fossil finds; (2) a halt in natural decay processes, a violation of actualism; (3) sheltering collagen from attack vectors (multiple dissimilar vectors make this unrealistic); and (4) the “iron model,” currently the most popular hypothesis. It posits that proteins are better preserved when they are cross-linked upon exposure to iron-rich fluids. Anderson steps through the problems with this model in a convincing, well-reasoned progression.

Anyone who wants an up-to-date, short (yet well-documented) summary of both secular and creationist research on this subject will find it here. *Echoes of the Jurassic* highlights the true nature of the worldview conflict, the desperate faith of secularists in the face of compelling evidence (naked empiricism is their epistemology, not ours), and another way in which God’s truth once again better defines reality in both past and present. Though not a technical monograph, this book is the outline of one, illustrating once more how science can be and is being reclaimed by its natural home of biblical Christianity.

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Instructions to Authors

Submission

Electronic submissions of all manuscripts and graphics are preferred and should be sent to the editor of the *Creation Research Society Quarterly* in Word, WordPerfect, or Star-Office/Open Office (see the inside front cover for address). Printed copies also are accepted. If submitting a printed copy, an original plus two copies of each manuscript should be sent to the editor. The manuscript and copies will not be returned to authors unless a stamped, self-addressed envelope accompanies submission. If submitting a manuscript electronically, a printed copy is not necessary unless specifically requested by the *Quarterly* editor. Manuscripts containing more than 35 pages (double-spaced and including references, tables, and figure legends) are discouraged. An author who determines that the topic cannot be adequately covered within this number of pages is encouraged to submit separate papers that can be serialized.

All submitted manuscripts will be reviewed by two or more technical referees. However, each section editor of the *Quarterly* has final authority regarding the acceptance of a manuscript for publication. While some manuscripts may be accepted with little or no modification, typically editors will seek specific revisions of the manuscript before acceptance. Authors will then be asked to submit revisions based upon comments made by the referees. In these instances, authors are encouraged to submit a detailed letter explaining changes made in the revision, and, if necessary, give reasons for not incorporating specific changes suggested by the editor or reviewer. If an author believes the rejection of a manuscript was not justified, an appeal may be made to the *Quarterly* editor (details of appeal process at the Society's web site, www.creationresearch.org).

Authors who are unsure of proper English usage should have their manuscripts checked by someone proficient in the English language. Also, authors should endeavor to make certain the manuscript (particularly the references) conforms to the style and format of the *Quarterly*. Manuscripts may be rejected on the basis of poor English or lack of conformity to the proper format.

The *Quarterly* is a journal of original writings, and only under unusual circumstances will previously published material be reprinted. Questions regarding this should be submitted to the Editor (CRSQeditor@creationresearch.org) prior to submitting any previously published material. In addition, manuscripts submitted to the *Quarterly* should not be concurrently submitted to another journal. Violation of this will result in immediate rejection of the submitted manuscript. Also, if an author uses copyrighted photographs or other material, a release from the copyright holder should be submitted.

Appearance

Manuscripts shall be computer-printed or neatly typed. Lines should be double-spaced, including figure legends, table footnotes, and references. All pages should be sequentially numbered. Upon acceptance of the manuscript for publication, an electronic version is requested (Word, WordPerfect, or Star-Office/Open Office), with the graphics in separate electronic files. However, if submission of an electronic final version is not possible for the author, then a cleanly printed or typed copy is acceptable.

Submitted manuscripts should have the following organizational format:

1. Title page. This page should contain the title of the manuscript, the author's name, and all relevant contact information (including mailing address, telephone number, fax number, and e-mail address). If the manuscript is submitted by multiple authors, one author should serve as the corresponding author, and this should be noted on the title page.

2. Abstract page. This is page 1 of the manuscript, and should contain the article title at the top, followed by the abstract for the article. Abstracts should be between 100 and 250 words in length and present an overview of the material discussed in the article, including all major conclusions. Use of abbreviations and references in the abstract should be avoided. This page should also contain at least five key words appropriate for identifying this article via a computer search.

3. Introduction. The introduction should provide sufficient background information to allow the reader to understand the relevance and significance of the article for creation science.

4. Body of the text. Two types of headings are typically used by the CRSQ. A major heading consists of a large font bold print that is centered in column, and is used for each major change of focus or topic. A minor heading consists of a regular font bold print that is flush to the left margin, and is used following a major heading and helps to organize points within each major topic. Do not split words with hyphens, or use all capital letters for any words. Also, do not use bold type, except for headings (italics can be occasionally used to draw distinction to specific words). Italics should not be used for foreign words in common usage, e.g., "et al.", "ibid.", "ca." and "ad infinitum." Previously published literature should be cited using the author's last name(s) and the year of publication (ex. Smith, 2003; Smith and Jones, 2003). If the citation has more than two authors, only the first author's name should appear (ex. Smith et al., 2003). Contributing authors should examine this issue of the CRSQ or consult the Society's web site for specific examples as well as a more detailed explanation of manuscript preparation. Frequently-used terms can be abbrevi-

ated by placing abbreviations in parentheses following the first usage of the term in the text, for example, polyacrylamide gel electrophoresis (PAGE) or catastrophic plate tectonics (CPT). Only the abbreviation need be used afterward. If numerous abbreviations are used, authors should consider providing a list of abbreviations. Also, because of the variable usage of the terms “microevolution” and “macroevolution,” authors should clearly define how they are specifically using these terms. Use of the term “creationism” should be avoided. All figures and tables should be cited in the body of the text, and be numbered in the sequential order that they appear in the text (figures and tables are numbered separately with Arabic and Roman numerals, respectively).

5. Summary. A summary paragraph(s) is often useful for readers. The summary should provide the reader an overview of the material just presented, and often helps the reader to summarize the salient points and conclusions the author has made throughout the text.

6. References. Authors should take extra measures to be certain that all references cited within the text are documented in the reference section. These references should be formatted in the current CRSQ style. (When the *Quarterly* appears in the references multiple times, then an abbreviation to CRSQ is acceptable.) The examples below cover the most common types of references:

Robinson, D.A., and D.P. Cavanaugh. 1998. A quantitative approach to baraminology with examples from the catarrhine primates. *CRSQ* 34:196–208.

Lipman, E.A., B. Schuler, O. Bakajin, and W.A. Eaton. 2003. Single-molecule measurement of protein folding kinetics. *Science* 301:1233–1235.

Margulis, L. 1971a. The origin of plant and animal cells. *American Scientific* 59:230–235.

Margulis, L. 1971b. *Origin of Eukaryotic Cells*. Yale University Press, New Haven, CT.

Hitchcock, A.S. 1971. *Manual of Grasses of the United States*. Dover Publications, New York, NY.

Walker, T.B. 1994. A biblical geologic model. In Walsh, R.E. (editor), *Proceedings of the Third International Conference on Creationism* (technical symposium sessions), pp. 581–592. Creation Science Fellowship, Pittsburgh, PA.

7. Tables. All tables cited in the text should be individually placed in numerical order following the reference section, and not embedded in the text. Each table should have a header statement that serves as a title for that table (see a current issue of the *Quarterly* for specific examples). Use tabs, rather than multiple spaces, in aligning columns within a table. Tables should be composed with *14-point type* to insure proper appearance in the columns of the *CRSQ*.

8. Figures. All figures cited in the text should be individually placed in numerical order, and placed after the tables. Do

not embed figures in the text. Each figure should contain a legend that provides sufficient description to enable the reader to understand the basic concepts of the figure without needing to refer to the text. Legends should be on a separate page from the figure. All figures and drawings should be of high quality (hand-drawn illustrations and lettering should be professionally done). Images are to be a minimum resolution of 300 dpi at 100% size. Patterns, not shading, should be used to distinguish areas within graphs or other figures. Unacceptable illustrations will result in rejection of the manuscript. Authors are also strongly encouraged to submit an electronic version (.cdr, .cpt, .gif, .jpg, and .tif formats) of all figures in individual files that are separate from the electronic file containing the text and tables.

Special Sections

Letters to the Editor:

Submission of letters regarding topics relevant to the Society or creation science is encouraged. Submission of letters commenting upon articles published in the *Quarterly* will be published two issues after the article's original publication date. Authors will be given an opportunity for a concurrent response. No further letters referring to a specific *Quarterly* article will be published. Following this period, individuals who desire to write additional responses/comments (particularly critical comments) regarding a specific *Quarterly* article are encouraged to submit their own articles to the *Quarterly* for review and publication.

Editor's Forum:

Occasionally, the editor will invite individuals to submit differing opinions on specific topics relevant to the *Quarterly*. Each author will have opportunity to present a position paper (2000 words), and one response (1000 words) to the differing position paper. In all matters, the editor will have final and complete editorial control. Topics for these forums will be solely at the editor's discretion, but suggestions of topics are welcome.

Book Reviews:

All book reviews should be submitted to the book review editor, who will determine the acceptability of each submitted review. Book reviews should be limited to 1000 words. Following the style of reviews printed in this issue, all book reviews should contain the following information: book title, author, publisher, publication date, number of pages, and retail cost. Reviews should endeavor to present the salient points of the book that are relevant to the issues of creation/evolution. Typically, such points are accompanied by the reviewer's analysis of the book's content, clarity, and relevance to the creation issue.

Creation Research Society

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Creation Research Society

History—The Creation Research Society was organized in 1963, with Dr. Walter E. Lammerts as first president and editor of a quarterly publication. Initially started as an informal committee of 10 scientists, it has grown rapidly, evidently filling a need for an association devoted to research and publication in the field of scientific creation, with a current membership of over 600 voting members (graduate degrees in science) and about 1000 non-voting members. The *Creation Research Society Quarterly* is a peer-reviewed technical journal. It has been gradually enlarged and modified, and is currently recognized as one of the outstanding publications in the field. In 1996 the CRSQ was joined by the newsletter *Creation Matters* as a source of information of interest to creationists.

Activities—The Society is a research and publication society, and also engages in various meetings and promotional activities. There is no affiliation with any other scientific or religious organizations. Its members conduct research on problems related to its purposes, and a research fund and research center are maintained to assist in such projects. Contributions to the research

fund for these purposes are tax deductible. As part of its vigorous research and field study programs, the Society operates The Van Andel Creation Research Center in Chino Valley, Arizona.

Membership—Voting membership is limited to scientists who have at least an earned graduate degree in a natural or applied science and subscribe to the Statement of Belief. Sustaining membership is available for those who do not meet the academic criterion for voting membership, but do subscribe to the Statement of Belief.

Statement of Belief—Members of the Creation Research Society, which include research scientists representing various fields of scientific inquiry, are committed to full belief in the biblical record of creation and early history, and thus to a concept of dynamic special creation (as opposed to evolution) both of the universe and the earth with its complexity of living forms. We propose to re-evaluate science from this viewpoint, and since 1964 have published a quarterly of research articles in this field. *All members of the Society subscribe to the following statement of belief:*

1. The Bible is the written Word of God, and because it is inspired throughout, all its assertions are historically and scientifically true in all the original autographs. To the student of nature this means that the account of origins in Genesis is a factual presentation of simple historical truths.

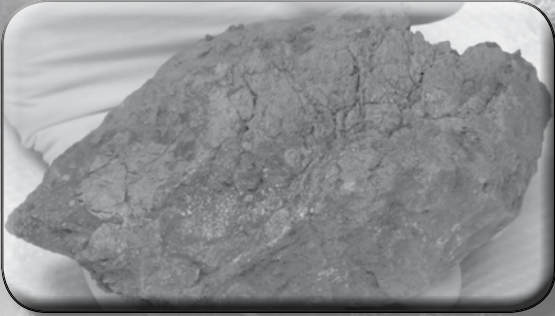
2. All basic types of living things, including humans, were made by direct creative acts of God during the Creation Week described in Genesis. Whatever biological changes have occurred since Creation Week have accomplished only changes within the original created kinds.

3. The Great Flood described in Genesis, commonly referred to as the Noachian Flood, was a historical event worldwide in its extent and effect.

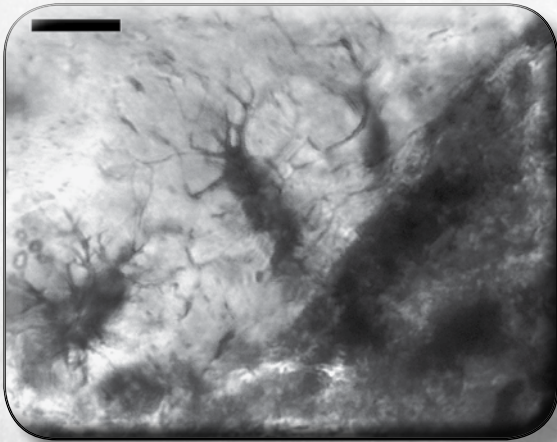
4. We are an organization of Christian men and women of science who accept Jesus Christ as our Lord and Savior. The act of the special creation of Adam and Eve as one man and woman and their subsequent fall into sin is the basis for our belief in the necessity of a Savior for all people. Therefore, salvation can come only through accepting Jesus Christ as our Savior.

iDINO II

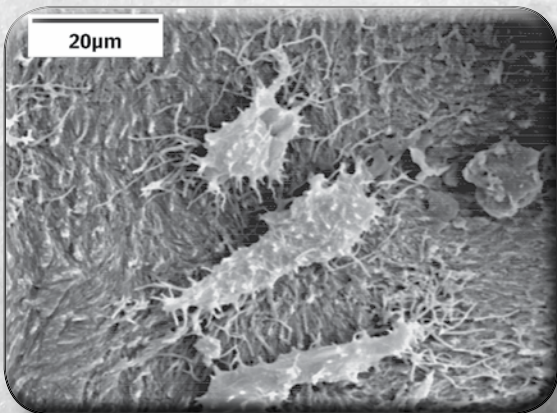
Investigation of Dinosaur Intact Natural Osteo-tissue



A fragment of the *Triceratops* brow horn.
Fragments, such as this one,
still contain tissue and cells.



Microscopic examination of tissue
extracted from a *Triceratops* horn
reveals bone cells still present.



Electron microscope picture of
intact bone cells still in tissue
extracted from a *Triceratops* horn.

How can pliable, stretchable tissue survive inside dinosaur fossils for over 65 million years?

How can this tissue still contain intact cells and even dinosaur proteins?

How can this fragile biological material survive for so long?

The answer to these questions directly challenges the current, evolutionary-biased, geologic timescale.

The Creation Research Society began its iDINO research initiative for the purpose of studying soft tissue in dinosaur fossils. The first phase of the project detected pliable, unfossilized tissue in a brow horn of a *Triceratops*. Within this tissue were intact osteocytes (bone cells). Some results from the iDINO project have been published in a technical microscopy journal and presented at an international microscopy conference. The Spring 2015 issue of the *Creation Research Society Quarterly* also features a special report of the iDINO project. Plus, to further spread the important information about soft tissue, the Society is developing a video (Echoes of the Jurassic).

The **second phase** of the project (iDINO II) will look more extensively at the process of tissue preservation. Evolutionists have offered various theories of how this tissue could survive for millions of years. iDINO II will methodically investigate these preservation claims, assessing their plausibility.

The iDINO results have already provided a strong challenge to the evolutionary worldview. More extensive and detailed examination may provide even stronger evidence that the age of dinosaur fossils is far less than 65 million years. To this end, the Society continues to seek those willing to fund this project with either one-time gifts or monthly donations.

For more information contact us at (928) 636-1153 or crsvarc@crsvarc.com.

Also visit <http://tinyurl.com/nphm2c4> for project updates and details.

